

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

83	7	2.6	282	20	RAY08328	M. grisea THNR pro	156	6	2.2	34	22	ABB27825	Human peptide #476
84	7	2.6	283	23	ABP04501	Staphylococcus epi	157	6	2.2	34	22	ABB32996	Peptide #502 enco
85	7	2.6	286	22	ABG3267	Pseudomonas aerugi	158	6	2.2	34	22	ABB42614	Peptide #10120 enc
86	7	2.6	298	21	ABG4787	Arabidopsis thalia	159	6	2.2	34	22	ABB18469	Protein #468 enco
87	7	2.6	298	21	ABG50312	Arabidopsis thalia	160	6	2.2	34	22	ABB37894	Human brain expres
88	7	2.6	308	22	ABG81589	S. epidermidis ope	161	6	2.2	34	22	AAAG53794	Human brain expres
89	7	2.6	311	23	ABP40326	Staphylococcus epi	162	6	2.2	34	22	AAAG66180	Human bone marrow
90	7	2.6	315	21	ABG50311	Staphylococcus epi	163	6	2.2	34	22	AAAG76319	Human bone marrow
91	7	2.6	316	21	ABG16294	Eucalyptus grandis	164	6	2.2	34	22	AAAG14051	Peptide #485 enco
92	7	2.6	316	21	ABG16321	Pinus radiata anne	165	6	2.2	34	22	AAAG26457	Peptide #473 enco
93	7	2.6	316	21	ABG24786	Arabidopsis thalia	166	6	2.2	34	22	AAAG01791	Human peptide enco
94	7	2.6	316	22	ABG5730	Annexin-like prote	167	6	2.2	34	22	ABG35830	H. pylori cytoplas
95	7	2.6	317	22	ABG5195	Drosophila melanog	168	6	2.2	37	18	AAW20245	Human prostate can
96	7	2.6	346	22	ABG71575	Drosophila melanog	169	6	2.2	37	22	AAU22783	Human reproductive
97	7	2.6	363	21	ABG08399	Arabidopsis thalia	170	6	2.2	37	22	AAAG4766	Human liver peptid
98	7	2.6	372	20	AAW88301	E. coli O157 antiq	171	6	2.2	38	22	ABG57627	Human secreted pro
99	7	2.6	372	20	AAW88301	E. coli O157 antiq	172	6	2.2	39	21	AAAB44596	Human secreted pro
100	7	2.6	384	23	ABG34138	Antibody productio	173	6	2.2	40	21	AAAB28737	Human secreted pro
101	7	2.6	387	22	ABG08398	Arabidopsis thalia	174	6	2.2	41	23	ABAB44709	Human protective s
102	7	2.6	407	22	ABG64058	Drosophila melanog	175	6	2.2	44	22	ABG29936	Novel human diagno
103	7	2.6	426	22	ABG1652	Drosophila melanog	176	6	2.2	46	19	AAW70327	Secreted protein F
104	7	2.6	426	22	ABG15281	Novel human diagno	177	6	2.2	46	22	ABG28111	Novel human diagno
105	7	2.6	429	21	AAI53802	47.7 kDa insectici	178	6	2.2	47	20	AAW73408	Human secreted pro
106	7	2.6	429	21	AAI53804	Insectical protein	179	6	2.2	48	20	AAI50889	Human secreted pro
107	7	2.6	439	21	AAI53808	Insectical protein	180	6	2.2	49	22	ABG57527	Human liver peptid
108	7	2.6	452	22	ABG70913	S cerevisiae apopt	181	6	2.2	49	22	ABG42096	Peptide #9602 enco
109	7	2.6	480	22	ABG05078	Drosophila melanog	182	6	2.2	49	22	AAAG52976	Human bone marrow
110	7	2.6	481	21	AAI58020	Aspergillus sojae	183	6	2.2	49	22	AAAG5789	Human bone marrow
111	7	2.6	481	24	ABU52604	Human NOVX protei	184	6	2.2	49	23	AAAG35899	Peptide #9936 enco
112	7	2.6	496	20	AAW89614	Aspergillus oryzae	185	6	2.2	49	23	ABG45259	Human peptide enco
113	7	2.6	496	20	AAW89597	Aspergillus oryzae	186	6	2.2	50	21	AAAG56198	Arabidopsis thalia
114	7	2.6	496	20	AAW89586	Aspergillus oryzae	187	6	2.2	50	21	AAAG56198	SIPI minimal Smad
115	7	2.6	550	22	ABG60941	Drosophila melanog	188	6	2.2	52	22	AAAG5784	Propionibacterium
116	7	2.6	569	22	AAU38295	Salmonella typhi c	189	6	2.2	53	19	AAI21383	Human HUPF-I mutan
117	7	2.6	573	21	AAI74962	Neisseria meningit	190	6	2.2	53	23	AAI21383	Human isomerase-li
118	7	2.6	575	21	AAI74961	Neisseria meningit	191	6	2.2	54	22	AAW70324	Human bone marrow
119	7	2.6	592	24	ABU00143	Human testis speci	192	6	2.2	54	22	AAW70324	Peptide #4597 enco
120	7	2.6	592	24	ABU00143	Human testis speci	193	6	2.2	54	22	AAAG5785	Peptide #4467 enco
121	7	2.6	614	20	AAW98112	T-cell membrane pr	194	6	2.2	55	23	ABG39970	Human peptide enco
122	7	2.6	614	20	AAW98113	T-cell membrane pr	195	6	2.2	55	23	ABG39970	Human musculoskele
123	7	2.6	634	22	ABG60004	Drosophila melanog	196	6	2.2	56	22	ABG03427	Novel human muscu
124	7	2.6	643	23	ABP41524	Human ovarian anti	197	6	2.2	56	22	ABU12721	Novel human peptid
125	7	2.6	822	19	AAW11943	Human OC-116 kDa p	198	6	2.2	56	22	AAU57140	Propionibacterium
126	7	2.6	822	23	ABG81811	Human OC-116 kDa p	199	6	2.2	56	22	AAU57140	Propionibacterium
127	7	2.6	824	23	AAU81516	Human interflagell	200	6	2.2	56	22	ABG38700	Propionibacterium
128	7	2.6	858	23	ABG2904	Herbicidally activ	201	6	2.2	56	22	ABG38700	Peptide #1351 enco
129	7	2.6	908	22	AAU36254	Pseudomonas aerugi	202	6	2.2	56	22	ABG3882	Peptide #1388 enco
130	7	2.6	1039	23	ABP66060	Bifidobacterium lo	203	6	2.2	56	22	ABG19323	Protein #1322 enco
131	7	2.6	1469	22	ABG68168	Drosophila melanog	204	6	2.2	56	22	AAAG4648	Human brain expres
132	7	2.6	1778	23	ABG47314	Listeria monocytog	205	6	2.2	56	22	AAAG4648	Human bone marrow
133	7	2.6	2705	22	AAW90772	Human shear stress	206	6	2.2	56	22	AAAG4648	Peptide #1348 enco
134	6	2.2	9	20	AAW81038	Melanoma associate	207	6	2.2	56	22	AAAG4648	Peptide #1322 enco
135	6	2.2	9	22	AAW81038	Melanoma associate	208	6	2.2	56	22	AAAG4648	Human prostate tum
136	6	2.2	11	22	AAW81038	OspA TC epitope ho	209	6	2.2	57	20	AAI74221	Human prostate tum
137	6	2.2	14	21	AAW99412	Staphylokinase T-C	210	6	2.2	58	22	AAU57783	Propionibacterium
138	6	2.2	17	22	AAW99401	Escherichia coli C	211	6	2.2	58	22	AAU57783	Propionibacterium
139	6	2.2	20	15	AAW5544	Staphylokinase var	212	6	2.2	58	22	AAU57783	Human EST encoded
140	6	2.2	20	16	AAW82493	Cry j i pollen all	213	6	2.2	59	23	AAU64157	Propionibacterium
141	6	2.2	20	20	AAW82493	Cry j i Japanese C	214	6	2.2	59	23	AAU64157	Propionibacterium
142	6	2.2	20	22	AAW82493	CJ linker library	215	6	2.2	61	21	AAAG56893	Human ORFX protein
143	6	2.2	21	22	ABG04204	Novel human diagno	216	6	2.2	62	22	ABG530025	Arabidopsis thalia
144	6	2.2	30	21	AAW92334	FIV gp36 envelope	217	6	2.2	62	22	ABG530025	Human liver peptid
145	6	2.2	31	19	AAW69836	Human neurofilamen	218	6	2.2	62	22	ABG530025	Human liver peptid
146	6	2.2	31	22	AAU31486	Novel human secret	219	6	2.2	62	22	ABG530025	Peptide #2634 enco
147	6	2.2	32	22	ABG5672	Human liver peptid	220	6	2.2	62	22	ABG530025	Peptide #2662 enco
148	6	2.2	32	22	ABG11303	Peptide #11809 enc	221	6	2.2	62	22	ABG530025	Peptide #5937 enco
149	6	2.2	32	22	ABG27165	Protein #5164 enco	222	6	2.2	62	22	ABG530025	Protein #5581 enco
150	6	2.2	32	22	AAW65340	Human brain expres	223	6	2.2	62	22	AAW5987	Human brain expres
151	6	2.2	32	22	AAW78035	Human bone marrow	224	6	2.2	62	22	AAW5987	Human bone marrow
152	6	2.2	32	22	AAW21926	Peptide #8360 enco	225	6	2.2	62	22	AAW68356	Human bone marrow
153	6	2.2	32	22	AAW38256	Peptide #12293 enc	226	6	2.2	62	22	AAW68356	Peptide #2808 enco
154	6	2.2	34	22	ABG47848	Human liver peptid	227	6	2.2	62	22	AAW68356	Peptide #2899 enco
155	6	2.2	34	22	ABG58029	Human liver peptid	228	6	2.2	62	22	AAW31870	Peptide #5907 enco

229	6	2.2	62	22	AA03901	Peptide #2583 enco	302	111	19	AAW61227	Streptococcus pneu
230	6	2.2	62	23	ABG37912	Human peptide enco	303	111	23	ABP54646	S. pneumoniae SP10
231	6	2.2	62	23	ABG41385	Human peptide enco	304	112	20	ABY36822	Amino acid sequenc
232	6	2.2	63	22	AAU63622	Propionibacterium	305	113	21	AGI15003	Arabidopsis thalia
233	6	2.2	63	23	ABP04955	Human ORFX protein	306	113	21	ABG11726	Novel human diagno
234	6	2.2	65	22	AGG99566	ERA binding domain	307	113	22	ABG44971	Zea mays protein f
235	6	2.2	66	21	AGS56892	Arabidopsis thalia	308	117	21	AGI2552	Zea mays protein f
236	6	2.2	66	23	ABP31177	Human histone-like	309	117	22	AAW23594	Macaque EST encode
237	6	2.2	67	22	ABG59870	Human liver peptid	310	117	22	AAW49273	Human RNA polymera
238	6	2.2	67	22	AAU42309	Propionibacterium	311	117	23	AAW49273	C glutamic prote
239	6	2.2	67	22	ABW44475	Peptide #11981 enc	312	118	22	AG92489	Humanised MAB heav
240	6	2.2	68	22	AAW05991	Human haematologic	313	119	14	AAW32240	Humanised MAB heav
241	6	2.2	68	22	AAW81957	Human haematologic	314	119	14	AAW32243	Humanised MAB heav
242	6	2.2	69	21	AGI17274	Arabidopsis thalia	315	119	14	AAW32244	Mature heavy chain
243	6	2.2	70	22	AAU57758	Propionibacterium	316	119	18	AAW27144	Humanised ABL 364
244	6	2.2	71	21	ABP64804	Human protein SEQ	317	119	22	AAW87570	Human AFP protein
245	6	2.2	72	21	ABG10911	Arabidopsis thalia	318	121	21	AG81441	Zea mays protein f
246	6	2.2	72	23	ABU05844	M. tuberculosis an	319	121	21	AG44980	Corynebacterium g1
247	6	2.2	73	22	AAU57812	Propionibacterium	320	121	23	ABP31114	Human glycoprotein
248	6	2.2	75	21	AGS32969	Arabidopsis thalia	321	122	21	AAW41174	Human ORFX ORF938
249	6	2.2	75	22	AAU39235	Propionibacterium	322	122	21	AG60092	Arabidopsis thalia
250	6	2.2	75	22	AAU46232	Propionibacterium	323	122	21	ABP04840	Human ORFX protein
251	6	2.2	75	22	ABW5913	Human nervous syst	324	123	14	AAW39152	Staphylokinase SAK
252	6	2.2	75	23	ABP03061	Human ORFX protein	325	123	21	AAW75507	Neisseria gonorrhoe
253	6	2.2	76	21	ABW59063	Breast and ovarian	326	123	21	AAW75508	Neisseria meningit
254	6	2.2	76	22	ABP04887	Human ORFX protein	327	123	21	AAW75509	Neisseria meningit
255	6	2.2	78	22	AAU54776	Propionibacterium	328	123	21	ABP26118	Streptococcus poly
256	6	2.2	78	22	AAU56637	Propionibacterium	329	126	13	AAW25458	Thrombolytic pepti
257	6	2.2	78	22	AAW74430	Human colon cancer	330	126	18	AAW20377	H. pylori surface
258	6	2.2	79	22	AAU39106	Propionibacterium	331	126	21	AGI23354	Zea mays protein f
259	6	2.2	80	21	AAW17273	Arabidopsis thalia	332	126	21	AAW123354	S. pneumoniae type
260	6	2.2	81	23	ABP09889	Human ORFX protein	333	126	24	ABU10162	Staphylokinase SAK
261	6	2.2	82	22	AAW57588	Human colon cancer	334	127	14	AAW39151	Human liver peptid
262	6	2.2	84	22	AAW64880	Murine protein SEQ	335	127	22	ABG52883	Human liver peptid
263	6	2.2	84	22	AAW64883	Murine protein SEQ	336	127	22	ABG38035	Peptide #5541 enco
264	6	2.2	84	23	ABP34514	Human ORFX protein	337	127	22	ABW23267	Protein #5266 enco
265	6	2.2	88	22	AAW57162	Human colon cancer	338	127	22	AAW71171	Human brain expres
266	6	2.2	89	22	AAO02868	Human polypeptide	339	127	22	AAW18909	Human bone marrow
267	6	2.2	89	23	ABP01213	Human ORFX protein	340	127	22	AAW311452	Peptide #5343 enco
268	6	2.2	90	18	AAW33889	Flea saliva protei	341	127	22	ABG40968	Peptide #5489 enco
269	6	2.2	90	19	AAW22363	Flea saliva protei	342	127	23	ABG40968	Human peptide enco
270	6	2.2	90	22	AAU61776	Propionibacterium	343	127	23	ABW89076	Human polypeptide
271	6	2.2	91	21	AAW14137	Bordetella pertuss	344	128	13	AAW29946	Deducted from Lelys
272	6	2.2	91	21	AAW10910	Arabidopsis thalia	345	128	16	AAW74643	PRRS virus (Spain)
273	6	2.2	91	21	AAW56246	Arabidopsis thalia	346	128	17	AAW94706	PRRS virus Lelystad ORF
274	6	2.2	91	23	ABP07609	Human ORFX protein	347	128	17	AAW88707	Porcine reproducti
275	6	2.2	92	22	ABW48734	Novel human diagno	348	128	19	AAW68456	PRRS isolate Tole
276	6	2.2	92	23	ABP06385	Human ORFX protein	349	128	20	AAW84335	Protein N of PRRSV
277	6	2.2	93	21	AAW40664	Human ORFX protein	350	128	22	ABW59767	Human liver peptid
278	6	2.2	94	22	AAW56996	Propionibacterium	351	128	22	AAW48122	Propionibacterium
279	6	2.2	95	23	ABW5791	Lactococcus lactis	352	128	22	AAW65460	Human brain expres
280	6	2.2	96	22	ABW14837	Novel human diagno	353	128	22	AAW38366	Peptide #12403 enc
281	6	2.2	96	22	AAO09550	Human polypeptide	354	128	22	AAU07139	Porcine reproducti
282	6	2.2	96	23	ABW10043	Human glucose tran	355	128	23	ABG96503	PRRS virus ORF7 pr
283	6	2.2	97	23	ABW97493	Novel human protei	356	128	23	ABG47145	Human peptide enco
284	6	2.2	99	23	ABP04383	Human ORFX protein	357	128	24	AAU76142	Porcine reproducti
285	6	2.2	101	23	ABP34284	Human kinase-like	358	128	24	ABP70395	Amino acid sequenc
286	6	2.2	101	23	ABP06196	Human ORFX protein	359	129	22	AAU59978	Propionibacterium
287	6	2.2	102	22	AAU07435	Flock house virus	360	129	22	ABW15536	Human nervous syst
288	6	2.2	102	23	AAU79657	Parietaria judaica	361	129	22	AAU18302	Human endocrine po
289	6	2.2	102	23	AAU79658	Parietaria judaica	362	130	21	AAW26892	Zea mays protein f
290	6	2.2	103	23	ABP39049	Staphylococcus epi	363	130	21	ABW1855	Drosophila melanog
291	6	2.2	104	22	AAU48120	Propionibacterium	364	131	17	AAW06934	CagI locus product
292	6	2.2	104	22	AAW60036	Propionibacterium	365	131	18	AAW20697	H. pylori putative
293	6	2.2	104	22	AAW80999	Human haematologic	366	131	20	AAW25608	Parietaria sp. all
294	6	2.2	104	22	AAW81968	Human haematologic	367	133	20	AAW25606	Parietaria sp. all
295	6	2.2	106	21	AAW58834	Arabidopsis thalia	368	133	23	ABP32750	Human RNA polymera
296	6	2.2	108	21	AAW54610	Zea mays protein f	369	135	21	AAW01298	Altered staphyloki
297	6	2.2	109	7	AAW60796	Fragment of sak ge	370	136	17	AAW03077	Staphylokinase der
298	6	2.2	109	21	AAW27841	Sequence homology	371	136	17	AAW03078	Staphylokinase der
299	6	2.2	109	21	AAW27842	Protein fragment e	372	136	17	AAW03082	Staphylokinase der
300	6	2.2	110	19	AAW98574	H. pylori GPO 27	373	136	17	AAW03083	Staphylokinase der
301	6	2.2	110	23	ABP00777	Human ORFX protein	374	136	17	AAW03080	Staphylokinase der

375	6	2.2	136	17	AAW03097	Staphylokinase der	448	6	2.2	136	20	AAV15049	Staphylokinase var
376	6	2.2	136	17	AAW03081	Staphylokinase der	449	6	2.2	136	20	AAV15050	Staphylokinase var
377	6	2.2	136	17	AAW03074	Staphylokinase der	450	6	2.2	136	20	AAV15061	Staphylokinase var
378	6	2.2	136	17	AAW03075	Staphylokinase der	451	6	2.2	136	20	AAV15060	Staphylokinase var
379	6	2.2	136	17	AAW03076	Staphylokinase der	452	6	2.2	136	20	AAV15037	Staphylokinase var
380	6	2.2	136	17	AAW03095	Staphylokinase der	453	6	2.2	136	20	AAV15022	Staphylokinase var
381	6	2.2	136	17	AAW03096	Staphylokinase der	454	6	2.2	136	20	AAV15023	Staphylokinase var
382	6	2.2	136	17	AAW03098	Staphylokinase der	455	6	2.2	136	20	AAV15038	Staphylokinase var
383	6	2.2	136	17	AAW03099	Staphylokinase der	456	6	2.2	136	20	AAV15024	Staphylokinase var
384	6	2.2	136	17	AAW03100	Staphylokinase der	457	6	2.2	136	20	AAV15054	Staphylokinase var
385	6	2.2	136	17	AAW03101	Staphylokinase der	458	6	2.2	136	20	AAV15025	Staphylokinase var
386	6	2.2	136	17	AAW03102	Staphylokinase der	459	6	2.2	136	20	AAV15039	Staphylokinase var
387	6	2.2	136	17	AAW03071	Wild-type staphylo	460	6	2.2	136	20	AAV15026	Staphylokinase var
388	6	2.2	136	17	AAW03072	Staphylokinase der	461	6	2.2	136	20	AAV15027	Staphylokinase var
389	6	2.2	136	17	AAW03073	Staphylokinase der	462	6	2.2	136	20	AAV15040	Staphylokinase var
390	6	2.2	136	17	AAW03093	Staphylokinase der	463	6	2.2	136	20	AAV15028	Staphylokinase var
391	6	2.2	136	17	AAW03090	Staphylokinase der	464	6	2.2	136	20	AAV15055	Staphylokinase var
392	6	2.2	136	17	AAW03094	Staphylokinase der	465	6	2.2	136	20	AAV15029	Staphylokinase var
393	6	2.2	136	17	AAW03103	Staphylokinase der	466	6	2.2	136	20	AAV15041	Staphylokinase var
394	6	2.2	136	17	AAW03104	Staphylokinase der	467	6	2.2	136	20	AAV15030	Staphylokinase var
395	6	2.2	136	17	AAW03087	Staphylokinase der	468	6	2.2	136	20	AAV15007	Staphylokinase var
396	6	2.2	136	17	AAW03088	Staphylokinase der	469	6	2.2	136	20	AAV15013	Staphylokinase var
397	6	2.2	136	17	AAW03089	Staphylokinase der	470	6	2.2	136	20	AAV15008	Staphylokinase var
398	6	2.2	136	17	AAW03091	Staphylokinase der	471	6	2.2	136	20	AAV15009	Staphylokinase var
399	6	2.2	136	17	AAW03092	Staphylokinase der	472	6	2.2	136	20	AAV15014	Staphylokinase var
400	6	2.2	136	17	AAW03084	Staphylokinase der	473	6	2.2	136	20	AAV15034	Staphylokinase var
401	6	2.2	136	17	AAW03085	Staphylokinase der	474	6	2.2	136	20	AAV15015	Staphylokinase var
402	6	2.2	136	17	AAW03086	Wild-type staphylo	475	6	2.2	136	20	AAV15016	Staphylokinase var
403	6	2.2	136	17	AAW03027	Staphylokinase der	476	6	2.2	136	20	AAV15035	Staphylokinase var
404	6	2.2	136	17	AAW03028	Staphylokinase der	477	6	2.2	136	20	AAV15018	Staphylokinase var
405	6	2.2	136	17	AAW03029	Staphylokinase der	478	6	2.2	136	20	AAV15019	Staphylokinase var
406	6	2.2	136	17	AAW03030	Staphylokinase der	479	6	2.2	136	20	AAV15036	Staphylokinase var
407	6	2.2	136	17	AAW03031	Staphylokinase der	480	6	2.2	136	20	AAV15020	Staphylokinase var
408	6	2.2	136	17	AAW44689	Staphylokinase mut	481	6	2.2	136	20	AAV15053	Staphylokinase var
409	6	2.2	136	19	AAW44696	Staphylokinase fro	482	6	2.2	136	20	AAV15021	Staphylokinase var
410	6	2.2	136	19	AAW44690	Staphylokinase mut	483	6	2.2	136	20	AAV15010	Staphylokinase var
411	6	2.2	136	19	AAW44691	Staphylokinase mut	484	6	2.2	136	20	AAV15002	Staphylokinase var
412	6	2.2	136	19	AAW44692	Staphylokinase mut	485	6	2.2	136	20	AAV15003	Staphylokinase var
413	6	2.2	136	19	AAW44693	Staphylokinase mut	486	6	2.2	136	20	AAV15011	Staphylokinase var
414	6	2.2	136	19	AAW44694	Staphylokinase mut	487	6	2.2	136	20	AAV15004	Staphylokinase var
415	6	2.2	136	19	AAW44695	Staphylokinase mut	488	6	2.2	136	20	AAV15032	Staphylokinase var
416	6	2.2	136	20	AAV15078	Staphylokinase var	489	6	2.2	136	20	AAV15005	Staphylokinase var
417	6	2.2	136	20	AAV15079	Staphylokinase var	490	6	2.2	136	20	AAV15012	Staphylokinase var
418	6	2.2	136	20	AAV15080	Staphylokinase var	491	6	2.2	136	20	AAV15006	Staphylokinase var
419	6	2.2	136	20	AAV15062	Staphylokinase var	492	6	2.2	136	20	AAV15033	Staphylokinase var
420	6	2.2	136	20	AAV15063	SakSTAR (K57A, E58	493	6	2.2	136	20	AAV01232	S. aureus staphylo
421	6	2.2	136	20	AAV15064	Staphylokinase var	494	6	2.2	136	21	AAO44284	Staphylococcus aur
422	6	2.2	136	20	AAV15065	Staphylokinase var	495	6	2.2	136	21	AAO44323	Arabidopsis thalia
423	6	2.2	136	20	AAV15066	SakSTAR (K35A, E65	496	6	2.2	136	21	AAO08768	Arabidopsis thalia
424	6	2.2	136	20	AAV15067	Staphylokinase var	497	6	2.2	136	21	AAO22478	Arabidopsis thalia
425	6	2.2	136	20	AAV15068	SakSTAR (B65D, K74	498	6	2.2	136	21	AAO43813	Arabidopsis thalia
426	6	2.2	136	20	AAV15069	SakSTAR (B65D, K74	499	6	2.2	136	21	AAO44415	Arabidopsis thalia
427	6	2.2	136	20	AAV15070	Staphylokinase var	500	6	2.2	136	21	AAO51295	Arabidopsis thalia
428	6	2.2	136	20	AAV15071	Staphylokinase var	501	6	2.2	136	21	AAO53099	Arabidopsis thalia
429	6	2.2	136	20	AAV15072	SakSTAR (K35A, E65	502	6	2.2	136	21	AAO53143	Arabidopsis thalia
430	6	2.2	136	20	AAV15073	Staphylokinase var	503	6	2.2	136	21	AAO53145	Arabidopsis thalia
431	6	2.2	136	20	AAV15074	Staphylokinase var	504	6	2.2	136	21	AAO58019	Arabidopsis thalia
432	6	2.2	136	20	AAV15075	Staphylokinase var	505	6	2.2	136	21	AAO1297	Wild type staphylo
433	6	2.2	136	20	AAV15076	Staphylokinase var	506	6	2.2	136	21	AAO99594	Staphylococcus pla
434	6	2.2	136	20	AAV15077	Staphylokinase var	507	6	2.2	136	21	AAV50871	Staphylococcus aur
435	6	2.2	136	20	AAV15078	Staphylokinase var	508	6	2.2	136	22	AAO99421	Staphylokinase (Sa
436	6	2.2	136	20	AAV15079	Staphylokinase var	509	6	2.2	136	22	AAO61908	S. aureus staphylo
437	6	2.2	136	20	AAV15081	Staphylokinase var	510	6	2.2	136	22	AAO61909	S. aureus staphylo
438	6	2.2	136	20	AAV15082	Staphylokinase var	511	6	2.2	136	23	AAO47321	Human dipeptide am
439	6	2.2	136	20	AAV15056	Staphylokinase var	512	6	2.2	136	23	AAO47900	Sak glucokinase.
440	6	2.2	136	20	AAV15043	Staphylokinase var	513	6	2.2	137	14	AAO39154	Staphylokinase SAK
441	6	2.2	136	20	AAV15057	Staphylokinase var	514	6	2.2	137	14	AAO39148	Staphylokinase SAK
442	6	2.2	136	20	AAV15045	Staphylokinase var	515	6	2.2	137	14	AAO39149	Staphylokinase SAK
443	6	2.2	136	20	AAV15046	Staphylokinase var	516	6	2.2	137	14	AAO39150	Staphylokinase SAK
444	6	2.2	136	20	AAV15058	Staphylokinase var	517	6	2.2	137	14	AAO39153	Staphylokinase SAK
445	6	2.2	136	20	AAV15047	Staphylokinase var	518	6	2.2	137	18	AAO33888	Flea saliva protei
446	6	2.2	136	20	AAV15048	Staphylokinase var	519	6	2.2	137	19	AAO82362	Staphylokinase
447	6	2.2	136	20	AAV15059	Staphylokinase var	520	6	2.2	137	20	AAV15051	SakSTAR (B65Q, K74



521	6	2, 2	137	20	AA15001	Staphylokinase gen	594	6	2, 2	156	22	AA05105	Peptide #3787 enco
522	6	2, 2	138	14	AAR32242	Chimeric MAB heavy	595	6	2, 2	157	21	AAG08767	Arabidopsis thalia
523	6	2, 2	138	14	AAR32246	BR55-2 murine IgG3	596	6	2, 2	157	21	AAG51262	Arabidopsis thalia
524	6	2, 2	138	22	ABG26002	Novel human diagno	597	6	2, 2	157	21	AAG53142	Arabidopsis thalia
525	6	2, 2	138	22	ABG26008	Novel human diagno	598	6	2, 2	157	22	AAG79850	Corynebacterium gl
526	6	2, 2	138	22	AAG90088	C glutamicum prote	599	6	2, 2	158	11	AA08285	Thermally stable c
527	6	2, 2	138	22	AAB92884	Human protein sequ	600	6	2, 2	158	12	AA08285	Staphylokinase-som
528	6	2, 2	139	14	AAR31588	BR55-2 heavy chain	601	6	2, 2	158	16	AA08285	Yeast cytosine-dea
529	6	2, 2	139	19	AAW56427	Amino end of the	602	6	2, 2	158	21	AA08285	Arabidopsis thalia
530	6	2, 2	140	21	AAB27795	Human secreted pro	603	6	2, 2	158	21	AA08285	Human secreted pro
531	6	2, 2	140	21	AA08285	Human secreted pro	604	6	2, 2	158	21	AA08285	Chimeric cytosine
532	6	2, 2	141	22	AAU39297	Propionibacterium	605	6	2, 2	158	21	AA08285	Chimeric cytosine
533	6	2, 2	141	22	AAU39297	Propionibacterium	606	6	2, 2	158	21	AA08285	Chimeric cytosine
534	6	2, 2	142	22	AAU39297	Propionibacterium	607	6	2, 2	158	21	AA08285	Chimeric cytosine
535	6	2, 2	143	22	AAU39297	Propionibacterium	608	6	2, 2	158	21	AA08285	Chimeric cytosine
536	6	2, 2	144	22	AAU39297	Propionibacterium	609	6	2, 2	158	21	AA08285	Chimeric cytosine
537	6	2, 2	145	21	AAU39297	Propionibacterium	610	6	2, 2	158	21	AA08285	Chimeric cytosine
538	6	2, 2	145	21	AAU39297	Propionibacterium	611	6	2, 2	158	21	AA08285	Chimeric cytosine
539	6	2, 2	145	21	AAU39297	Propionibacterium	612	6	2, 2	158	21	AA08285	Chimeric cytosine
540	6	2, 2	145	21	AAU39297	Propionibacterium	613	6	2, 2	158	21	AA08285	Chimeric cytosine
541	6	2, 2	145	21	AAU39297	Propionibacterium	614	6	2, 2	158	21	AA08285	Chimeric cytosine
542	6	2, 2	145	21	AAU39297	Propionibacterium	615	6	2, 2	158	21	AA08285	Chimeric cytosine
543	6	2, 2	146	21	AAU39297	Propionibacterium	616	6	2, 2	158	21	AA08285	Chimeric cytosine
544	6	2, 2	146	21	AAU39297	Propionibacterium	617	6	2, 2	158	21	AA08285	Chimeric cytosine
545	6	2, 2	146	21	AAU39297	Propionibacterium	618	6	2, 2	158	21	AA08285	Chimeric cytosine
546	6	2, 2	146	21	AAU39297	Propionibacterium	619	6	2, 2	158	21	AA08285	Chimeric cytosine
547	6	2, 2	146	21	AAU39297	Propionibacterium	620	6	2, 2	158	21	AA08285	Chimeric cytosine
548	6	2, 2	146	21	AAU39297	Propionibacterium	621	6	2, 2	158	21	AA08285	Chimeric cytosine
549	6	2, 2	147	21	AAU39297	Propionibacterium	622	6	2, 2	158	21	AA08285	Chimeric cytosine
550	6	2, 2	147	21	AAU39297	Propionibacterium	623	6	2, 2	158	21	AA08285	Chimeric cytosine
551	6	2, 2	148	21	AAU39297	Propionibacterium	624	6	2, 2	158	21	AA08285	Chimeric cytosine
552	6	2, 2	148	21	AAU39297	Propionibacterium	625	6	2, 2	158	21	AA08285	Chimeric cytosine
553	6	2, 2	148	21	AAU39297	Propionibacterium	626	6	2, 2	158	21	AA08285	Chimeric cytosine
554	6	2, 2	148	21	AAU39297	Propionibacterium	627	6	2, 2	158	21	AA08285	Chimeric cytosine
555	6	2, 2	148	21	AAU39297	Propionibacterium	628	6	2, 2	158	21	AA08285	Chimeric cytosine
556	6	2, 2	148	21	AAU39297	Propionibacterium	629	6	2, 2	158	21	AA08285	Chimeric cytosine
557	6	2, 2	148	21	AAU39297	Propionibacterium	630	6	2, 2	158	21	AA08285	Chimeric cytosine
558	6	2, 2	148	21	AAU39297	Propionibacterium	631	6	2, 2	158	21	AA08285	Chimeric cytosine
559	6	2, 2	148	21	AAU39297	Propionibacterium	632	6	2, 2	158	21	AA08285	Chimeric cytosine
560	6	2, 2	148	21	AAU39297	Propionibacterium	633	6	2, 2	158	21	AA08285	Chimeric cytosine
561	6	2, 2	148	21	AAU39297	Propionibacterium	634	6	2, 2	158	21	AA08285	Chimeric cytosine
562	6	2, 2	148	21	AAU39297	Propionibacterium	635	6	2, 2	158	21	AA08285	Chimeric cytosine
563	6	2, 2	148	21	AAU39297	Propionibacterium	636	6	2, 2	158	21	AA08285	Chimeric cytosine
564	6	2, 2	148	21	AAU39297	Propionibacterium	637	6	2, 2	158	21	AA08285	Chimeric cytosine
565	6	2, 2	148	21	AAU39297	Propionibacterium	638	6	2, 2	158	21	AA08285	Chimeric cytosine
566	6	2, 2	148	21	AAU39297	Propionibacterium	639	6	2, 2	158	21	AA08285	Chimeric cytosine
567	6	2, 2	148	21	AAU39297	Propionibacterium	640	6	2, 2	158	21	AA08285	Chimeric cytosine
568	6	2, 2	149	21	AAU39297	Propionibacterium	641	6	2, 2	158	21	AA08285	Chimeric cytosine
569	6	2, 2	149	21	AAU39297	Propionibacterium	642	6	2, 2	158	21	AA08285	Chimeric cytosine
570	6	2, 2	149	21	AAU39297	Propionibacterium	643	6	2, 2	158	21	AA08285	Chimeric cytosine
571	6	2, 2	150	20	AAU39297	Propionibacterium	644	6	2, 2	158	21	AA08285	Chimeric cytosine
572	6	2, 2	150	20	AAU39297	Propionibacterium	645	6	2, 2	158	21	AA08285	Chimeric cytosine
573	6	2, 2	151	21	AAU39297	Propionibacterium	646	6	2, 2	158	21	AA08285	Chimeric cytosine
574	6	2, 2	151	21	AAU39297	Propionibacterium	647	6	2, 2	158	21	AA08285	Chimeric cytosine
575	6	2, 2	151	21	AAU39297	Propionibacterium	648	6	2, 2	158	21	AA08285	Chimeric cytosine
576	6	2, 2	151	21	AAU39297	Propionibacterium	649	6	2, 2	158	21	AA08285	Chimeric cytosine
577	6	2, 2	151	21	AAU39297	Propionibacterium	650	6	2, 2	158	21	AA08285	Chimeric cytosine
578	6	2, 2	152	21	AAU39297	Propionibacterium	651	6	2, 2	158	21	AA08285	Chimeric cytosine
579	6	2, 2	152	21	AAU39297	Propionibacterium	652	6	2, 2	158	21	AA08285	Chimeric cytosine
580	6	2, 2	152	21	AAU39297	Propionibacterium	653	6	2, 2	158	21	AA08285	Chimeric cytosine
581	6	2, 2	152	21	AAU39297	Propionibacterium	654	6	2, 2	158	21	AA08285	Chimeric cytosine
582	6	2, 2	153	21	AAU39297	Propionibacterium	655	6	2, 2	158	21	AA08285	Chimeric cytosine
583	6	2, 2	154	18	AAU39297	Propionibacterium	656	6	2, 2	158	21	AA08285	Chimeric cytosine
584	6	2, 2	154	21	AAU39297	Propionibacterium	657	6	2, 2	158	21	AA08285	Chimeric cytosine
585	6	2, 2	154	21	AAU39297	Propionibacterium	658	6	2, 2	158	21	AA08285	Chimeric cytosine
586	6	2, 2	154	21	AAU39297	Propionibacterium	659	6	2, 2	158	21	AA08285	Chimeric cytosine
587	6	2, 2	155	22	AAU39297	Propionibacterium	660	6	2, 2	158	21	AA08285	Chimeric cytosine
588	6	2, 2	156	21	AAU39297	Propionibacterium	661	6	2, 2	158	21	AA08285	Chimeric cytosine
589	6	2, 2	156	21	AAU39297	Propionibacterium	662	6	2, 2	158	21	AA08285	Chimeric cytosine
590	6	2, 2	156	21	AAU39297	Propionibacterium	663	6	2, 2	158	21	AA08285	Chimeric cytosine
591	6	2, 2	156	21	AAU39297	Propionibacterium	664	6	2, 2	158	21	AA08285	Chimeric cytosine
592	6	2, 2	156	21	AAU39297	Propionibacterium	665	6	2, 2	158	21	AA08285	Chimeric cytosine
593	6	2, 2	156	21	AAU39297	Propionibacterium	666	6	2, 2	158	21	AA08285	Chimeric cytosine

667	6	2.2	203	22	ABB30559	Peptide #3210 enco	740	6	2.2	245	21	AAB43361	Human ORFX ORF3125
668	6	2.2	203	22	ABB33724	Peptide #3230 enco	741	6	2.2	245	21	AAG29538	Arabidopsis thalia
669	6	2.2	203	22	ABB21550	Protein #3149 enco	742	6	2.2	245	22	AAB73692	Human oxidoreducta
670	6	2.2	203	22	AAM26533	Human brain expres	743	6	2.2	245	22	AAB84368	Amino acid sequenc
671	6	2.2	203	22	AAM68915	Human bone marrow	744	6	2.2	245	22	AAG78802	Short-chain dehydr
672	6	2.2	203	22	AAM16738	Peptide #3172 enco	745	6	2.2	245	23	ABP43639	21615 ADH. Homo s
673	6	2.2	203	22	AAM23226	Peptide #3263 enco	746	6	2.2	245	23	ABG34070	Human pro peptide
674	6	2.2	203	22	AAM04455	Peptide #3137 enco	747	6	2.2	245	23	AAU76224	Human 21615 alcoh
675	6	2.2	203	23	ABG38495	Human peptide enco	748	6	2.2	246	19	AAW54386	Actinomadura hibis
676	6	2.2	203	23	ABP41242	Human ovarian anti	749	6	2.2	246	21	AAV91422	Human secreted pro
677	6	2.2	203	24	AAU05173	Human expressed pr	750	6	2.2	246	22	AAB63575	Human gastric can
678	6	2.2	204	22	AAB63960	Human prostate can	751	6	2.2	247	21	AAG10126	Arabidopsis thalia
679	6	2.2	206	22	ABE66042	Drosophila melanog	752	6	2.2	247	22	ABE68065	Drosophila melanog
680	6	2.2	206	23	AAU91312	Human protein NOVI	753	6	2.2	248	23	ABP27440	Streptococcus poly
681	6	2.2	207	22	AAG82967	S. epidermidis ope	754	6	2.2	248	23	AAW34409	Lactobacillus coli p
682	6	2.2	209	21	AAG59510	Arabidopsis thalia	755	6	2.2	251	18	AAV34891	Chlamydia pneumonia
683	6	2.2	211	19	AAW81141	A Histplasma capsu	756	6	2.2	251	20	AAV34891	Chlamydia pneumonia
684	6	2.2	211	24	AAU00128	Human novel polype	757	6	2.2	251	22	ABE65238	Drosophila melanog
685	6	2.2	212	24	ABJ26853	Thymidylate synth	758	6	2.2	252	22	AAB96231	Putative P. abysssi
686	6	2.2	214	23	AAU23332	Novel human enzyme	759	6	2.2	252	23	AAW47358	Recombinant mosqui
687	6	2.2	214	23	ABW77428	Human tumour marke	760	6	2.2	253	19	AAV17437	Aed a 3 CDNA clone
688	6	2.2	215	21	AAW57361	Arabidopsis thalia	761	6	2.2	253	20	AAV17437	Arabidopsis thalia
689	6	2.2	220	21	AAB21244	MMGPV partial fuso	762	6	2.2	253	21	AAG29537	Arabidopsis thalia
690	6	2.2	220	22	ABE63373	Drosophila melanog	763	6	2.2	253	22	ABE64081	Drosophila melanog
691	6	2.2	220	22	AAW59043	C glutamicum prote	764	6	2.2	253	22	AAU34686	E. coli cellular p
692	6	2.2	220	22	ABE63373	Human polypeptide	765	6	2.2	253	22	AAU38285	Salmonella typhi c
693	6	2.2	221	22	ABE63341	Drosophila melanog	766	6	2.2	253	22	AAU32078	Propionibacterium
694	6	2.2	223	21	AAU29539	Arabidopsis thalia	767	6	2.2	253	23	AAU31054	Arabidopsis trans
695	6	2.2	224	22	AAU81711	Novel central nerv	768	6	2.2	254	22	ABW8981	Drosophila melanog
696	6	2.2	224	22	AAU43520	Human polypeptide	769	6	2.2	254	22	ABP30228	C. glutamicum SPT
697	6	2.2	224	22	AAU19935	Novel human calciu	770	6	2.2	254	23	AAU39509	Streptococcus poly
698	6	2.2	225	21	AAG14316	Arabidopsis thalia	771	6	2.2	255	21	AAG59509	Arabidopsis thalia
699	6	2.2	225	21	ABE63449	Drosophila melanog	772	6	2.2	255	21	ABE62988	Drosophila melanog
700	6	2.2	226	19	AAW73397	Staphylococcus aur	773	6	2.2	256	23	ABJ10953	Yeast selected int
701	6	2.2	230	22	ABE58344	Drosophila melanog	774	6	2.2	257	22	ABG51845	Human liver peptid
702	6	2.2	230	22	AAU54317	Propionibacterium	775	6	2.2	257	22	ABE59275	Drosophila melanog
703	6	2.2	230	23	ABP30530	Streptococcus poly	776	6	2.2	257	22	ABW70701	Drosophila melanog
704	6	2.2	231	23	ABP28562	Streptococcus poly	777	6	2.2	257	22	AAU36113	Klebsiella pneumon
705	6	2.2	232	21	AAG40276	Arabidopsis thalia	778	6	2.2	257	22	AAU46230	Propionibacterium
706	6	2.2	232	22	ABE58317	Drosophila melanog	779	6	2.2	257	22	ABW17699	Peptide #4420 enco
707	6	2.2	235	21	AAW43848	Human cancer assoc	780	6	2.2	257	22	ABW36995	Peptide #4501 enco
708	6	2.2	235	21	AAW45276	Novel human enzyme	781	6	2.2	257	22	ABW32310	Protein #4309 enco
709	6	2.2	236	21	ABG45276	Protein fragment #	782	6	2.2	257	22	AAW57723	Human brain expres
710	6	2.2	236	22	ABG09577	Novel human diagn	783	6	2.2	257	22	AAW70135	Human bone marrow
711	6	2.2	237	23	ABG72187	Human zinc finger	784	6	2.2	257	22	AAW17969	Peptide #4403 enco
712	6	2.2	239	21	AAU7529	Arabidopsis thalia	785	6	2.2	257	22	AAW30473	Peptide #4510 enco
713	6	2.2	239	22	ABW5337	Propionibacterium	786	6	2.2	257	22	AAW05604	Peptide #4286 enco
714	6	2.2	239	22	ABW5337	Human protein sequ	787	6	2.2	257	23	ABG39774	Human peptide enco
715	6	2.2	239	22	ABW5736	Human protein sequ	788	6	2.2	258	21	AAV32318	Arabidopsis thalia
716	6	2.2	239	23	ABW94029	Arabidopsis thalia	789	6	2.2	260	21	AAV32318	Arabidopsis thalia
717	6	2.2	239	23	ABW94029	Human polypeptide	790	6	2.2	260	23	ABG56534	Human short chain
718	6	2.2	239	23	AAE15248	Human RNA metaboli	791	6	2.2	261	23	AAE20115	Lactobacillus rham
719	6	2.2	240	21	AAG13229	Arabidopsis thalia	792	6	2.2	262	21	AAG29142	Arabidopsis thalia
720	6	2.2	240	21	ABP65279	Bifidobacterium lo	793	6	2.2	262	22	ABE69111	Drosophila melanog
721	6	2.2	241	10	AAU90060	N-terminal sequenc	794	6	2.2	263	22	ABE52576	Escherichia coli p
722	6	2.2	241	12	AAU10679	Acetoacetyl CoA re	795	6	2.2	263	23	ABP28167	Streptococcus poly
723	6	2.2	241	18	AAW26128	Flagellin excretor	796	6	2.2	264	24	ABP60424	Lactobacillus kefi
724	6	2.2	241	21	AAW58902	Breast and ovarian	797	6	2.2	264	24	AAO19611	Human nucleic acid
725	6	2.2	242	21	AAW38843	Human Blys binding	798	6	2.2	265	21	AAG07323	Arabidopsis thalia
726	6	2.2	242	23	ABW45873	Lactococcus lactis	799	6	2.2	265	21	AAG29141	Arabidopsis thalia
727	6	2.2	242	23	ABW55221	Streptococcus poly	800	6	2.2	265	21	AAG52633	Arabidopsis thalia
728	6	2.2	243	20	ABW27345	Human prostate can	801	6	2.2	266	21	AAG33466	Arabidopsis thalia
729	6	2.2	244	20	AAV48390	Streptococcus pneu	802	6	2.2	266	21	AAG35505	Arabidopsis thalia
730	6	2.2	244	21	AAV81721	Amino acid sequenc	803	6	2.2	267	21	AAV94890	Human protein clon
731	6	2.2	244	21	AAV4421	E. coli cellular p	804	6	2.2	267	21	AAV94890	Human secreted pro
732	6	2.2	244	22	AAU34533	E. coli cellular p	805	6	2.2	267	22	ABE68874	Human RECAP polype
733	6	2.2	244	22	AAU34533	Salmonella typhi c	806	6	2.2	267	22	ABE68874	Novel human secret
734	6	2.2	244	22	AAU38298	Human novel cytoki	807	6	2.2	268	22	AAU31169	H. pylori ORF hpa
735	6	2.2	244	22	AAU68551	Human novel cytoki	808	6	2.2	269	16	AAU55694	Bifidobacterium lo
736	6	2.2	244	23	AAU10969	Poly3-hydroxybutan	809	6	2.2	269	23	ABP58877	Arabidopsis thalia
737	6	2.2	244	23	ABG6548	Human short chain	810	6	2.2	270	22	ABE68846	Drosophila melanog
738	6	2.2	244	24	AAU01873	S. pneumoniae type	811	6	2.2	271	22	AAU49489	Propionibacterium
739	6	2.2	245	18	AAW55497	H. pylori ORF 01ge	812	6	2.2	272	23	ABP38019	Staphylococcus epi

813	6	2.2	273	10	AAP94155	Acetyl-CoA reducta	886	2.2	302	23	ABB55540	Lactococcus lactis
814	6	2.2	273	12	AAR13141	B.burgdorferi str	887	2.2	304	21	AAAG10125	Arabidopsis thalia
815	6	2.2	273	16	AAR75733	B31/Pgau outer sur	888	2.2	304	21	AAG38842	Arabidopsis thalia
816	6	2.2	273	16	AAR75724	B.burgdorferi str	889	2.2	307	20	AAW83373	Streptococcus pneu
817	6	2.2	273	21	AAG40275	Arabidopsis thalia	890	2.2	307	23	ABP65479	Bifidobacterium lo
818	6	2.2	273	23	AAU79603	Borrelia strain PG	891	2.2	308	21	AAAB42901	Human ORFX ORF265
819	6	2.2	273	23	AAU79612	Borrelia OspA-B31/	892	2.2	308	21	AAG35504	Arabidopsis thalia
820	6	2.2	273	23	AAU91490	Outer surface prot	893	2.2	309	22	AAG71525	Human olfactory re
821	6	2.2	273	23	AAU91493	Outer surface prot	894	2.2	309	23	ABJ04029	Human G-protein co
822	6	2.2	274	22	AAU38991	Human polypeptide	895	2.2	309	23	ABB90219	Human polypeptide
823	6	2.2	274	23	AAO22161	Ramoplanin biosynt	896	2.2	309	23	ABBS3928	Lactococcus lactis
824	6	2.2	275	21	ABG15500	Arabidopsis thalia	897	2.2	310	22	AAU35114	Enterococcus faeca
825	6	2.2	275	22	ABB60233	Drosophila melanog	898	2.2	311	23	ABP60861	Helicobacter pylor
826	6	2.2	275	22	ABB92468	Human protein sequ	899	2.2	311	23	ABP60862	Helicobacter pylor
827	6	2.2	275	23	ABB93346	Herbicidally activ	900	2.2	312	23	ABP51656	Human MAP kinase p
828	6	2.2	276	22	AAU19523	Human diagnostic a	901	2.2	313	23	ABP64798	Human protein SEQ
829	6	2.2	276	22	ABP28780	Streptococcus poly	902	2.2	313	23	ABBS3515	Lactococcus lactis
830	6	2.2	277	21	AAG04192	Arabidopsis thalia	903	2.2	314	20	AAW88347	Salmonella enteric
831	6	2.2	277	21	AAG12731	Arabidopsis thalia	904	2.2	314	22	AAB83955	Amino acid sequenc
832	6	2.2	277	23	ABB93346	Herbicidally activ	905	2.2	314	23	ABB94333	Chlamydia pneumoni
833	6	2.2	278	21	AAU96729	PRO1800. a Hep27 h	906	2.2	315	17	AAR89323	Rape leaf beta-ket
834	6	2.2	278	21	AAU68735	Short chain alcoho	907	2.2	315	17	AAR89322	Rape seed beta-ket
835	6	2.2	278	22	AAB93414	Human protein sequ	908	2.2	315	19	AAW61616	Clone HMCR70 of I
836	6	2.2	278	23	ABG31395	Human PRO1800 poly	909	2.2	315	21	AAG36461	Arabidopsis thalia
837	6	2.2	278	23	ABG13955	Novel human secret	910	2.2	315	23	ABP60866	Mycoplasma pneumon
838	6	2.2	278	23	ABG92703	Human secreted pro	911	2.2	316	23	ABP65646	Bifidobacterium lo
839	6	2.2	278	23	AAU86157	Human PRO1800 poly	912	2.2	316	23	ABG66824	Human prostate spe
840	6	2.2	278	24	ABU60807	Human secreted/tra	913	2.2	317	21	AAG08874	Arabidopsis thalia
841	6	2.2	278	24	ABG73308	Human PRO1800 poly	914	2.2	317	21	AAG09200	Arabidopsis thalia
842	6	2.2	279	22	AAG90188	C glutamicum prote	915	2.2	317	23	AAE22736	MAP kinase phosphat
843	6	2.2	280	21	AAG14532	Arabidopsis thalia	916	2.2	318	18	AAW18337	Murine liver p32 1
844	6	2.2	280	22	ABB58639	Drosophila melanog	917	2.2	318	20	AAU02004	A retinol dehydrog
845	6	2.2	280	22	ABU931983	Human protein sequ	918	2.2	319	21	AAU10905	S. aureus hydroxic
846	6	2.2	281	23	ABBS3574	Lactococcus lactis	919	2.2	319	21	AAU10124	Arabidopsis thalia
847	6	2.2	282	21	AAU91301	Group B Streptococ	920	2.2	320	22	AAU60254	Propionibacterium
848	6	2.2	282	23	ABP73909	Candida albicans e	921	2.2	320	22	AAW78980	C. glutamicum SRT
849	6	2.2	283	22	ABG62175	Drosophila melanog	922	2.2	320	23	ABB49122	Listeria monocytog
850	6	2.2	284	22	ABB66010	Drosophila melanog	923	2.2	321	21	AAG28323	Arabidopsis thalia
851	6	2.2	284	22	AAU67996	Propionibacterium	924	2.2	322	20	AAU74098	Human prostate tum
852	6	2.2	286	22	AAU34096	Staphylococcus aur	925	2.2	322	21	AAU36460	Arabidopsis thalia
853	6	2.2	286	22	AAU87080	Staphylococcus aur	926	2.2	322	23	ABP59845	Human polypeptide
854	6	2.2	287	14	AAR35435	Staphylococcus aur	927	2.2	322	23	AAU35884	Helicobacter pylor
855	6	2.2	287	22	AAG74298	B. burgdorferi str	928	2.2	323	22	AAU00481	S. galli laeus dTDP
856	6	2.2	287	22	AAG81687	Human colon cancer	929	2.2	323	23	ABU52037	Helicobacter pylor
857	6	2.2	288	9	AAP2051	S. epidermidis ope	930	2.2	325	20	AAU02465	Polypeptide isolat
858	6	2.2	288	20	AAU29081	Cl-inhibitor. Uni	931	2.2	325	22	AAU24632	Human olfactory re
859	6	2.2	288	20	AAU29082	T. gondii immunoge	932	2.2	325	22	AAU24632	Corynebacterium gl
860	6	2.2	288	22	AAU25552	T. gondii immunoge	933	2.2	325	23	ABP95749	Human GPCR polypep
861	6	2.2	288	22	AAU25553	T. gondii immunoge	934	2.2	325	23	AAU95611	Human olfactory an
862	6	2.2	290	22	ABB52563	Escherichia coli p	935	2.2	325	23	AAU85252	G-coupled olfactor
863	6	2.2	290	24	ABP78330	N. gonorrhoeae ami	936	2.2	325	24	ABP72220	Human G-protein co
864	6	2.2	292	21	AAU96266	K. aestuarii carbo	937	2.2	326	18	AAW21022	H. pylori cytoplasm
865	6	2.2	292	22	AAG92082	C glutamicum prote	938	2.2	326	21	AAU70153	Staphylococcus aur
866	6	2.2	293	22	AAU36606	Staphylococcus aur	939	2.2	326	22	ABB64046	Drosophila melanog
867	6	2.2	293	22	AAG82270	S. epidermidis ope	940	2.2	326	23	AAE25702	Staphylococcus aur
868	6	2.2	294	22	ABB69041	Drosophila melanog	941	2.2	327	21	AAU43417	Human cancer assoc
869	6	2.2	294	23	ABU49569	Actinoplanes sp ac	942	2.2	327	21	AAG09199	Arabidopsis thalia
870	6	2.2	294	23	ABU49566	Listeria monocytog	943	2.2	328	21	AAG08873	Arabidopsis thalia
871	6	2.2	294	24	ABU25625	Aspergillus fumiga	944	2.2	328	21	AAU52389	Human transmembran
872	6	2.2	295	22	AAU36240	Pseudomonas aerugi	945	2.2	329	23	ABP28231	Streptococcus poly
873	6	2.2	295	22	AAU79400	Corynebacterium gl	946	2.2	330	18	AAW20625	H. pylori cytoplasm
874	6	2.2	295	22	AAU79401	Corynebacterium gl	947	2.2	330	22	AAU36613	Human FLEXHT-35 pr
875	6	2.2	295	23	ABP39214	Staphylococcus epi	948	2.2	331	19	AAW46748	Human granulocytic
876	6	2.2	296	20	AAU23799	A gyrase protein s	949	2.2	331	23	ABU49260	Listeria monocytog
877	6	2.2	296	20	AAU34800	Chlamydia pneumoni	950	2.2	332	20	AAU42333	Staphylococcus aur
878	6	2.2	296	21	AAU96270	K. aestuarii carbo	951	2.2	332	20	AAU31826	Staphylococcus aur
879	6	2.2	296	22	AAG92779	C glutamicum prote	952	2.2	332	22	AAU39371	Human polypeptide
880	6	2.2	296	22	AAG81281	Human APP protein	953	2.2	332	22	AAU41157	Human polypeptide
881	6	2.2	297	22	AAU23504	Novel human enzyme	954	2.2	332	22	AAG93303	Human protein HP10
882	6	2.2	297	22	AAU17597	Novel signal trans	955	2.2	332	22	AAU94250	Human protein sequ
883	6	2.2	298	22	AAG82115	S. epidermidis ope	956	2.2	332	22	AAU94873	Human protein sequ
884	6	2.2	300	23	ABU48784	Listeria monocytog	957	2.2	332	23	AAE15246	Human RNA metaboli
885	6	2.2	301	21	AAG59508	Arabidopsis thalia	958	2.2	333	22	AAU30724	Novel human secret



KW (-)-trachelogenin; antiviral; (-)-podophyllotoxin.

OS Forsythia intermedia.

XX WO9955846-A1.

XX 04-NOV-1999.

XX 23-APR-1999; 99WO-US08975.

XX 24-APR-1998; 98US-0082977.

XX (UNIV ) UNIV WASHINGTON STATE RES FOUND.

XX Xia Z, Costa MA, Davin LB, Lewis NG;

XX WPI; 2000-126356/11.

XX N-PSDB; AAZ45743.

PT New nucleic acid molecule encoding an enzyme involved in lignan biosynthetic pathway, useful for producing large amounts of lignans

XX Example 2; Page 61-63; 66pp; English.

XX The present sequence represents a secoisolariciresinol dehydrogenase protein. The enzyme is involved in the lignan biosynthetic pathway. The secoisolariciresinol dehydrogenase proteins have a molecular weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require NAD or NADP as a cofactor. The secoisolariciresinol dehydrogenase nucleic acids are used for the recombinant expression of the enzymes. It is also used to obtain expression or enhanced expression of secoisolariciresinol dehydrogenase in plants or to alter lignan biosynthesis. The enzyme is used for production of the pharmacologically active lignan, matairesinol. The secoisolariciresinol dehydrogenase proteins and nucleic acids can be utilized to: elevate or otherwise alter the levels of health-protecting lignans, including phytoestrogens such as enterolactone and enterodiol, in plant species, including vegetables, grains and fruits and to food items incorporating material derived from such genetically altered plants; genetically alter plant species to provide an abundant, natural supply of lignans useful for a variety of purposes, for example as nutraceuticals and dietary supplements; to genetically alter living organisms to produce an abundant supply of optically pure lignans having desirable biological properties, for example (-)-trachelogenin which possesses antiviral properties, and (-)-podophyllotoxin.

XX Sequence 272 AA;

Query Match 99.6%; Score 272; DB 21; Length 272;

Best Local Similarity 100.0%; Pred. No. 1.6e-269;

Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QLRTAFARLEGKVALITGGASIGGETTAKLFSQHGAKVAIADVQDELGHSVWEAIGTSN 61

Db 1 QLRTAFARLEGKVALITGGASIGGETTAKLFSQHGAKVAIADVQDELGHSVWEAIGTSN 60

Qy 62 STYIHCVDVTNEDGVKNADVNTVSTYGLKDIMFNSNAGISDPNRPRIIDNEKADPERVLSVN 121

Db 61 STYIHCVDVTNEDGVKNADVNTVSTYGLKDIMFNSNAGISDPNRPRIIDNEKADPERVLSVN 120

Qy 122 VTGVFLCMKHAARVMIPARSGNIISTASLSSTMTGGSSSHAYCGSKHVAIATRLNLADELG 181

Db 121 VTGVFLCMKHAARVMIPARSGNIISTASLSSTMTGGSSSHAYCGSKHVAIATRLNLADELG 180

Qy 182 QFGIRVNCLSPFGLPTALGKFKFSIGKNEEPEENVINPAGNLKGPKNVEDVANAAIYLAS 241

Db 181 QFGIRVNCLSPFGLPTALGKFKFSIGKNEEPEENVINPAGNLKGPKNVEDVANAAIYLAS 240

Qy 242 DEAKVVSGHNLFIDGGFSVCNSVVKVFOYRDS 273

Db 241 DEAKVVSGHNLFIDGGFSVCNSVVKVFOYRDS 272

RESULT 3

AAAY54413

ID AAY54413 standard; Protein; 277 AA.

XX AC AAY54413;

XX 06-APR-2000 (first entry)

XX Secoisolariciresinol dehydrogenase protein clone SMDBHY321.

XX Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway; lignan; matairesinol; health-protecting lignan; phytoestrogen; enterolactone; enterodiol; nutraceutical; dietary supplement; (-)-trachelogenin; antiviral; (-)-podophyllotoxin.

OS Forsythia intermedia.

XX WO9955846-A1.

XX 04-NOV-1999.

XX 23-APR-1999; 99WO-US08975.

XX 24-APR-1998; 98US-0082977.

XX (UNIV ) UNIV WASHINGTON STATE RES FOUND.

XX Xia Z, Costa MA, Davin LB, Lewis NG;

XX WPI; 2000-126356/11.

XX N-PSDB; AAZ45731.

PT New nucleic acid molecule encoding an enzyme involved in lignan biosynthetic pathway, useful for producing large amounts of lignans

XX Claim 8; Page 49-50; 66pp; English.

XX The present sequence represents a secoisolariciresinol dehydrogenase protein. The enzyme is involved in the lignan biosynthetic pathway. The secoisolariciresinol dehydrogenase proteins have a molecular weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require NAD or NADP as a cofactor. The secoisolariciresinol dehydrogenase nucleic acids are used for the recombinant expression of the enzymes. It is also used to obtain expression or enhanced expression of secoisolariciresinol dehydrogenase in plants or to alter lignan biosynthesis. The enzyme is used for production of the pharmacologically active lignan, matairesinol. The secoisolariciresinol dehydrogenase proteins and nucleic acids can be utilized to: elevate or otherwise alter the levels of health-protecting lignans, including phytoestrogens such as enterolactone and enterodiol, in plant species, including vegetables, grains and fruits and to food items incorporating material derived from such genetically altered plants; genetically alter plant species to provide an abundant, natural supply of lignans useful for a variety of purposes, for example as nutraceuticals and dietary supplements; to genetically alter living organisms to produce an abundant supply of optically pure lignans having desirable biological properties, for example (-)-trachelogenin which possesses antiviral properties, and (-)-podophyllotoxin.

XX Sequence 277 AA;

Query Match 40.3%; Score 110; DB 21; Length 277;

Best Local Similarity 100.0%; Pred. No. 7.9e-104;

Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ARRLGKVALITGGASIGGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSNITYHC 67

Db 12 ARRLGKVALITGGASIGGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSNITYHC 71

Qy 68 DVTNEDGVKNADVNTVSTYGLKDIMFNSNAGISDPNRPRIIDNEKADPERV 117

Db 72 DVTNEDGVKNADVNTVSTYGLKDIMFNSNAGISDPNRPRIIDNEKADPERV 121

```

RESULT 4
AAV5414
ID AAY54414 standard; Protein; 273 AA.
AC AAY54414;
XX
DT 06-APR-2000 (first entry)
XX
DE Secoisolaricresinol dehydrogenase protein clone SMDEHY431.
XX
KW Secoisolaricresinol dehydrogenase; lignan biosynthetic pathway;
KW lignan; matairesinol; health-protecting lignan; phytoestrogen;
KW enterolactone; enterodiol; neutriceutical; dietary supplement;
KW (-)-trachelogenin; antiviral; (-)-podophyllotoxin.
XX
OS Forsythia intermedia.
XX
FH Key Location/Qualifiers
FT Misc-difference 120 /note= "encoded by GTN"
FT Misc-difference 122 /note= "encoded by GTN"
FT
FT
FT
XX WO9955846-A1.
XX
PD 04-NOV-1999.
XX
PF 23-APR-1999; 99WO-US089975.
XX
PR 24-APR-1998; 98US-0082977.
XX
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.
XX
PI Xia Z, Costa MA, Davin LB, Lewis NG;
XX
DR WPI; 2000-126356/11.
XX
DR N-PSDB; AAZ45732.
XX
PT New nucleic acid molecule encoding an enzyme involved in lignan
PT biosynthetic pathway, useful for producing large amounts of lignans
PS Claim 8; Page 51-52; 66pp; English.
XX
XX
XX The present sequence represents a secoisolaricresinol dehydrogenase
XX protein. The enzyme is involved in the lignan biosynthetic pathway.
XX The secoisolaricresinol dehydrogenase proteins have a molecular
XX weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require
XX NAD or NADP as a cofactor. The secoisolaricresinol dehydrogenase
XX nucleic acids are used for the recombinant expression of the enzymes.
XX It is also used to obtain expression or enhanced expression of
XX secoisolaricresinol dehydrogenase in plants or to alter lignan
XX biosynthesis. The enzyme is used for production of the pharmacologically
XX active lignan, matairesinol. The secoisolaricresinol dehydrogenase
XX proteins and nucleic acids can be utilized to: elevate or otherwise
XX alter the levels of health-protecting lignans, including phytoestrogens
XX such as enterolactone and enterodiol, in plant species, including
XX vegetables, grains and fruits and to food items incorporating material
XX derived from such genetically altered plants; genetically alter plant
XX species to provide an abundant, natural supply of lignans useful for
XX a variety of purposes, for example as nutraceuticals and dietary
XX supplements; to genetically alter living organisms to produce an
XX abundant supply of optically pure lignans having desirable biological
XX properties, for example (-)-trachelogenin which possesses antiviral
XX properties, and (-)-podophyllotoxin.
XX
XX Sequence 273 AA;
XX
Query Match 12.5%; Score 34; DB 21; Length 273;
Best Local Similarity 100.0%; Pred. No. 4.2e-26;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 60 SNSTYIHCDDVTNEDGVKNAVDNTVSTYKGLDIMP 93
Db 60 SNSTYIHCDDVTNEDGVKNAVDNTVSTYKGLDIMP 93

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|||||
Db 60 SNSTYIHCDDVTNEDGVKNAVDNTVSTYKGLDIMP 93
|||||
RESULT 5
AAV54416
ID AAY54416 standard; Protein; 276 AA.
AC AAY54416;
XX
DT 06-APR-2000 (first entry)
XX
DE Secoisolaricresinol dehydrogenase protein clone SMDEHY631.
XX
KW Secoisolaricresinol dehydrogenase; lignan biosynthetic pathway;
KW lignan; matairesinol; health-protecting lignan; phytoestrogen;
KW enterolactone; enterodiol; neutriceutical; dietary supplement;
KW (-)-trachelogenin; antiviral; (-)-podophyllotoxin.
XX
OS Forsythia intermedia.
XX
PN WO9955846-A1.
XX
PD 04-NOV-1999.
XX
PF 23-APR-1999; 99WO-US089975.
XX
PR 24-APR-1998; 98US-0082977.
XX
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.
XX
PI Xia Z, Costa MA, Davin LB, Lewis NG;
XX
DR WPI; 2000-126356/11.
XX
DR N-PSDB; AAZ45734.
XX
PT New nucleic acid molecule encoding an enzyme involved in lignan
PT biosynthetic pathway, useful for producing large amounts of lignans
PS Claim 8; Page 56-57; 66pp; English.
XX
XX
XX The present sequence represents a secoisolaricresinol dehydrogenase
XX protein. The enzyme is involved in the lignan biosynthetic pathway.
XX The secoisolaricresinol dehydrogenase proteins have a molecular
XX weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require
XX NAD or NADP as a cofactor. The secoisolaricresinol dehydrogenase
XX nucleic acids are used for the recombinant expression of the enzymes.
XX It is also used to obtain expression or enhanced expression of
XX secoisolaricresinol dehydrogenase in plants or to alter lignan
XX biosynthesis. The enzyme is used for production of the pharmacologically
XX active lignan, matairesinol. The secoisolaricresinol dehydrogenase
XX proteins and nucleic acids can be utilized to: elevate or otherwise
XX alter the levels of health-protecting lignans, including phytoestrogens
XX such as enterolactone and enterodiol, in plant species, including
XX vegetables, grains and fruits and to food items incorporating material
XX derived from such genetically altered plants; genetically alter plant
XX species to provide an abundant, natural supply of lignans useful for
XX a variety of purposes, for example as nutraceuticals and dietary
XX supplements; to genetically alter living organisms to produce an
XX abundant supply of optically pure lignans having desirable biological
XX properties, for example (-)-trachelogenin which possesses antiviral
XX properties, and (-)-podophyllotoxin.
XX
XX Sequence 276 AA;
XX
Query Match 12.5%; Score 34; DB 21; Length 276;
Best Local Similarity 100.0%; Pred. No. 4.3e-26;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 60 SNSTYIHCDDVTNEDGVKNAVDNTVSTYKGLDIMP 93
Db 63 SNSTYIHCDDVTNEDGVKNAVDNTVSTYKGLDIMP 96

```

RESULT 6  
 AAO21494  
 ID AAO21494 standard; Protein; 276 AA.  
 XX  
 AC AAO21494;  
 AC  
 DT 15-AUG-2002. (first entry)  
 XX  
 DE  
 XX  
 XX  
 KW Secoisolariciresinol dehydrogenase protein.  
 KW Guaiacyl (G)-lignan; monocytyledon plant; rice; food additive;  
 KW seed-specific transcriptional regulatory region; dehydrogenase; enzyme.  
 XX  
 OS Unidentified.  
 OS  
 XX WO200220548-A1.  
 PN  
 XX 14-MAR-2002.  
 PD  
 XX  
 XX 04-SEP-2001; 2001WO-US27500.  
 PF  
 XX  
 XX 07-SEP-2000; 2000US-230632P.  
 PR  
 XX  
 XX (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
 FA (PHYT-) APPLIED PHYTOLOGICS INC.  
 PA  
 XX  
 XX Lewis NG, Davin LB, Huang N;  
 PI  
 XX WPI; 2002-425767/45.  
 DR  
 XX N-PSDB; AAL38432.  
 DR  
 XX  
 XX Increasing guaiacyl-lignan content in monocytyledon plants, by  
 PT transforming plant with chimeric gene construct having seed-specific  
 PT transcriptional regulator linked to gene encoding protein involved in  
 PT G-lignan formation  
 XX  
 XX Claim 2; Fig 10; 136pp; English.  
 PS  
 XX  
 XX The invention relates to a method for increasing the guaiacyl (G)-lignan  
 CC content in seeds of a monocytyledon plant, comprising selecting at least  
 CC one protein or enzyme integral to the pathway leading to G-lignan  
 CC formation, stably transforming a monocytyledon plant with chimeric gene  
 CC (CG) constructs having a seed-specific transcriptional regulatory region  
 CC operably linked to a nucleic acid sequence encoding the enzyme. The  
 CC method of the invention is useful for stably transforming a  
 CC monocytyledonous plant (e.g. rice) with CG constructs resulting in  
 CC increased expression of the genes encoded by CG constructs. The G-lignan  
 CC enriched seed composition is useful as a food additive. This  
 CC sequence represents the secoisolariciresinol dehydrogenase protein  
 CC relating to the invention.  
 XX  
 SQ Sequence 276 AA;  
 Query Match 12.5%; Score 34; DB 23; Length 276;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-26;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 60 SNSTYIHCVDVTNEDGVKNVADNTVSTYTKLDIMF 93  
 DB 63 SNSTYIHCVDVTNEDGVKNVADNTVSTYTKLDIMF 96  
 RESULT 7  
 AAY54415  
 ID AAY54415 standard; Protein; 277 AA.  
 XX  
 AC AAY54415;  
 AC  
 DT 06-APR-2000 (first entry)  
 XX  
 DE  
 XX Secoisolariciresinol dehydrogenase protein clone SMDEHY511.  
 DE  
 XX

KW Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway;  
 KW lignan; matairesinol; health-protecting lignan; phytoestrogen;  
 KW enterolactone; enterodiol; neutriceutical; dietary supplement;  
 KW (-)-trachelogenin; antiviral; (-)-podophyllotoxin.  
 XX  
 OS Forsythia intermedia.  
 OS  
 XX WO9955846-A1.  
 PN  
 XX 04-NOV-1999.  
 PD  
 XX  
 XX 23-APR-1999; 99WO-US08975.  
 PF  
 XX  
 XX 24-APR-1998; 98US-0082977.  
 PR  
 XX  
 XX (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
 PA  
 XX  
 XX Xia Z, Costa WA, Davin LB, Lewis NG;  
 PI  
 XX WPI; 2000-126356/11.  
 DR  
 XX N-PSDB; AAZ45733.  
 DR  
 XX  
 XX New nucleic acid molecule encoding an enzyme involved in lignan  
 PT biosynthetic pathway, useful for producing large amounts of lignans  
 PT  
 XX  
 XX Claim 8; Page 54-55; 66pp; English.  
 PS  
 XX  
 XX The present sequence represents a secoisolariciresinol dehydrogenase  
 CC protein. The enzyme is involved in the lignan biosynthetic pathway.  
 CC The secoisolariciresinol dehydrogenase proteins have a molecular  
 CC weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require  
 CC NAD or NADP as a cofactor. The secoisolariciresinol dehydrogenase  
 CC nucleic acids are used for the recombinant expression of the enzymes.  
 CC It is also used to obtain expression or enhanced expression of  
 CC secoisolariciresinol dehydrogenase in plants or to alter lignan  
 CC biosynthesis. The enzyme is used for production of the pharmacologically  
 CC active lignan, matairesinol. The secoisolariciresinol dehydrogenase  
 CC proteins and nucleic acids can be utilized to: elevate or otherwise  
 CC alter the levels of health-protecting lignans, including phytoestrogens  
 CC such as enterolactone and enterodiol, in plant species, including  
 CC vegetables, grains and fruits and to food items incorporating material  
 CC derived from such genetically altered plants; genetically alter plant  
 CC species to provide an abundant, natural supply of lignans useful for  
 CC a variety of purposes, for example as nutraceuticals and dietary  
 CC supplements; to genetically alter living organisms to produce an  
 CC abundant supply of optically pure lignans having desirable biological  
 CC properties, for example (-)-trachelogenin which possesses antiviral  
 CC properties, and (-)-podophyllotoxin.  
 XX  
 SQ Sequence 277 AA;  
 Query Match 12.5%; Score 34; DB 21; Length 277;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-26;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 29 TAKLFSQHGAIAADVDQDELGHVVEAIGTSNS 62  
 DB 33 TAKLFSQHGAIAADVDQDELGHVVEAIGTSNS 66  
 RESULT 8  
 AAY54418  
 ID AAY54418 standard; Peptide; 17 AA.  
 XX  
 AC AAY54418;  
 AC  
 DT 06-APR-2000 (first entry)  
 XX  
 DE Trypsin fragment of a secoisolariciresinol dehydrogenase protein.  
 DE  
 XX Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway;  
 KW lignan; matairesinol; health-protecting lignan; phytoestrogen;  
 KW enterolactone; enterodiol; neutriceutical; dietary supplement;  
 KW

KW (-)-trachelogenin; antiviral; (-)-podophyllotoxin.  
 XX Forsythia intermedia.  
 XX WO955846-A1.  
 XX 04-NOV-1999.  
 XX 23-APR-1999; 99WO-US08975.  
 XX 24-APR-1998; 98US-0082977.  
 XX (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
 XX Xia Z, Costa MA, Davin LB, Lewis NG;  
 XX WPI; 2000-126356/11.  
 XX New nucleic acid molecule encoding an enzyme involved in lignan  
 XX biosynthetic pathway, useful for producing large amounts of lignans -  
 XX Example 1; Page 58, 66pp; English.  
 XX The present sequence represents a peptide of a secoisolariciresinol  
 XX dehydrogenase. The enzyme is involved in the lignan biosynthetic pathway.  
 XX The secoisolariciresinol dehydrogenase proteins have a molecular  
 XX weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require  
 XX NAD or NADP as a cofactor. The secoisolariciresinol dehydrogenase  
 XX nucleic acids are used for the recombinant expression of the enzymes.  
 XX It is also used to obtain expression or enhanced expression of  
 XX secoisolariciresinol dehydrogenase in plants or to alter lignan  
 XX biosynthesis. The enzyme is used for production of the pharmacologically  
 XX active lignan, matairesinol. The secoisolariciresinol dehydrogenase  
 XX proteins and nucleic acids can be utilized to: elevate or otherwise  
 XX alter the levels of health-protecting lignans, including phytoestrogens  
 XX such as enterolactone and enterodiol, in plant species, including  
 XX vegetables, grains and fruits and to food items incorporating material  
 XX derived from such genetically altered plants; genetically alter plant  
 XX species to provide an abundant, natural supply of lignans useful for  
 XX a variety of purposes, for example as nutraceuticals and dietary  
 XX supplements; to genetically alter living organisms to produce an  
 XX abundant supply of optically pure lignans having desirable biological  
 XX properties, for example (-)-trachelogenin which possesses antiviral  
 XX properties, and (-)-podophyllotoxin.  
 XX Sequence 17 AA;  
 XX  
 XX Query Match 6.2%; Score 17; DB 21; Length 17;  
 XX Best Local Similarity 100.0%; Pred. No. 7.6e-10;  
 XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 15 VALITGASGIGTTAK 31  
 Db 1 VALITGASGIGTTAK 17  
 RESULT 9  
 AAG31552  
 ID AAG31552 standard; Protein; 283 AA.  
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 XX AAG31552;  
 XX 17-OCT-2000 (first entry)  
 XX Arabidopsis thaliana protein fragment SEQ ID NO: 37910.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 37910.  
 KW Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.  
 XX Arabidopsis thaliana.  
 OS Arabidopsis thaliana.  
 XX EP1033405-A2.  
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 XX 06-SEP-2000.  
 XX 25-FEB-2000; 2000EP-0301439.  
 XX 25-FEB-1999; 99US-0121825.  
 XX 05-MAR-1999; 99US-0123180.  
 XX 09-MAR-1999; 99US-0123548.  
 XX 23-MAR-1999; 99US-0125788.  
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 XX 07-JUN-1999; 99US-0137724.  
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 XX 29-JUN-1999; 99US-0140891.  
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 XX 01-JUL-1999; 99US-0141842.  
 XX 01-JUL-1999; 99US-0142154.  
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PR 02-JUL-1999; 99US-0142055.  
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PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LEGKVALITGGAGIG 26  
Db 18 LEGKVALITGGAGIG 33

RESULT 10  
ABB92823

ID ABB92823 standard; Protein; 283 AA.

XX ABB92823;

XX 31-MAY-2002 (first entry)

DT Herbicidally active polypeptide SEQ ID NO 2034.

DE Herbicidal; plant; agriculture; herbicide.

KW Arabidopsis thaliana.

XX WO200210210-A2.

XX 07-FEB-2002.

XX 28-AUG-2001; 2001WO-EP09892.

XX 28-AUG-2001; 2001WO-EP09892.

XX (FARB ) BAYER AG.

XX

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PI Tietjen K, Weidler M;
XX WPI; 2002-269010/31.
XX
XX Identifying plant target proteins for herbicidally active compounds.
PT comprising aligning and comparing nucleic acid or amino acid sequences
PT from plant with nucleic acid or amino acid sequences from non-plant
PT organisms -
XX
XX Claim 5; SEQ ID NO 2034; 261pp + Sequence Listing; English.
XX
XX The invention relates to identifying target proteins
CC (ABB90790-ABB94016) for herbicidally active compounds, comprising
CC aligning and comparing nucleic acid or amino acid sequences from plant
CC with nucleic acid or amino acid sequences from non-plant organisms using
CC suitable search parameters, where plant sequences having an E-value
CC greater by a factor of 3 than the E-value of most similar non-plant
CC sequences are selected. The polypeptides or nucleic acids encoding them
CC are useful for identifying modulators. The identified modulators are
CC useful as herbicides.
XX
XX Sequence 283 AA;
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Query Match 5.9%; Score 16; DB 23; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.le-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 18 LEGKVALITGGASGIG 33
RESULT 11
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XX 17-OCT-2000 (first entry)
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XX Arabidopsis thaliana protein fragment SEQ ID NO: 20101.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
OS
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XX 06-SEP-2000.
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XX 25-FEB-2000; 2000EP-0301439.
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XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
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PR 07-OCT-1999; 99US-0158023.
PR 08-OCT-1999; 99US-0158233.
PR 12-OCT-1999; 99US-0158369.
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PR 14-OCT-1999; 99US-0159637.
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Query Match 5.9%; Score 16; DB 21; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LEGKVALITGGASGIG 26
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AC AAG18619;
XX
DT 17-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 20100.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
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PR 29-OCT-1999; 99US-0162142.

Query Match 5.9%; Score 16; DB 21; Length 343;  
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Qy 11 LEGKVALITGGASGIG 26  
Db 78 LEGKVALITGGASGIG 93

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ID ABB92449 standard; Protein; 280 AA.  
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AC ABB92449;  
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DT 31-MAY-2002 (first entry)

XX Herbicidally active polypeptide SEQ ID NO 1660.

XX Herbicidal; plant; agriculture; herbicide.

XX Arabidopsis thaliana.

XX WO200210210-A2.

XX 07-FEB-2002.

XX 28-AUG-2001; 2001WO-EP09892.

XX 28-AUG-2001; 2001WO-EP09892.

XX (FARB ) BAYER AG.

XX Tietjen K, Weidler M;

XX WPI; 2002-269010/31.

XX Identifying plant target proteins for herbicidally active compounds,  
XX comprising aligning and comparing nucleic acid or amino acid sequences  
XX from plant with nucleic acid or amino acid sequences from non-plant  
XX organisms -

XX Claim 5; SEQ ID NO 1660; 261pp + Sequence Listing; English.

XX The invention relates to identifying target proteins  
XX (ABB90790-ABB94016) for herbicidally active compounds, comprising  
XX aligning and comparing nucleic acid or amino acid sequences from plant  
XX with nucleic acid or amino acid sequences from non-plant organisms using  
XX suitable search parameters, where plant sequences having an E-value  
XX greater by a factor of 3 than the E-value of most similar non-plant  
XX sequences are selected. The polypeptides or nucleic acids encoding them  
XX are useful for identifying modulators. The identified modulators are  
XX useful as herbicides.

XX Sequence 280 AA;

Query Match 5.1%; Score 14; DB 23; Length 280;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LEGKVALITGGASG 24

Db 15 LEGKVALITGGASG 28

RESULT 14  
AAY54419  
ID AAY54419 standard; Peptide; 15 AA.

XX  
AC AAY54419;

XX  
DT 06-APR-2000 (first entry)

XX Trypsin fragment of a secoisolariciresinol dehydrogenase protein.

XX Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway;  
XX lignan; matairesinol; health-protecting lignan; phytoestrogen;  
XX enterolactone; enterodiol; neutriceutical; dietary supplement;  
XX (-)-trachelogenin; antiviral; (-)-podophyllotoxin.

XX Forsythia intermedia.

XX WO9955846-A1.

XX 04-NOV-1999.

XX 23-APR-1999; 99WO-US08975.

XX 24-APR-1998; 98US-0082977.

XX (UNIW ) UNIV WASHINGTON STATE RES FOUND.

XX Xia Z, Costa MA, Davin LB, Lewis NG;

XX WPI; 2000-126356/11.

XX New nucleic acid molecule encoding an enzyme involved in lignan  
XX biosynthetic pathway, useful for producing large amounts of lignans

XX Example 1; Page 58; 66pp; English.

XX The present sequence represents a peptide of a secoisolariciresinol  
XX dehydrogenase. The enzyme is involved in the lignan biosynthetic pathway.  
XX The secoisolariciresinol dehydrogenase proteins have a molecular  
XX weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require  
XX NAD or NADP as a cofactor. The secoisolariciresinol dehydrogenase  
XX nucleic acids are used for the recombinant expression of the enzymes.  
XX It is also used to obtain expression or enhanced expression of  
XX secoisolariciresinol dehydrogenase in plants or to alter lignan  
XX biosynthesis. The enzyme is used for production of the pharmacologically  
XX active lignan, matairesinol. The secoisolariciresinol dehydrogenase  
XX proteins and nucleic acids can be utilized to: elevate or otherwise  
XX alter the levels of health-protecting lignans, including phytoestrogens  
XX such as enterolactone and enterodiol, in plant species, including  
XX vegetables, grains and fruits and to food items incorporating material  
XX derived from such genetically altered plants; genetically alter plant  
XX species to provide an abundant, natural supply of lignans useful for  
XX a variety of purposes, for example as neutraceuticals and dietary  
XX supplements; to genetically alter living organisms to produce an  
XX abundant supply of optically pure lignans having desirable biological  
XX properties, for example (-)-trachelogenin which possesses antiviral  
XX properties, and (-)-podophyllotoxin.

XX Sequence 15 AA;

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Best Local Similarity 100.0%; Pred. No. 8.8e-05;  
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Qy 91 IMFSNAGISDPN 102

Db 3 IMFSNAGISDPN 14

RESULT 15

ABP00547

ID ABP00547 standard; Protein; 127 AA.

XX AC ABP00547;  
 XX XX  
 XX DT 25-JUN-2002 (first entry)  
 XX DE Human ORFX protein sequence SEQ ID NO:1076.  
 XX KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;  
 KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;  
 KW degenerative disorder; osteoarthritis; neurodegenerative disorder;  
 KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;  
 KW hypertension; hypothyroidism; cholesterol ester storage disease;  
 KW immune deficiency; immune disorder; infectious disease;  
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;  
 KW myasthenia gravis.  
 XX OS Homo sapiens.  
 XX XX  
 XX FN WO200192523-A2.  
 XX XX  
 XX PD 06-DEC-2001.  
 XX XX  
 XX PF 29-MAY-2001; 2001WO-US10836.  
 XX XX  
 XX PR 30-MAY-2000; 2000US-206132P.  
 XX PR 29-AUG-2000; 2000US-228716P.  
 XX XX  
 XX PA (CURA-) CURAGEN CORP.  
 XX XX  
 XX PI Shimkets RA, Leach MD;  
 XX DR WPI; 2002-106308/14.  
 XX DR N-PSDB; ABN16299.  
 XX XX  
 XX PT Novel human polypeptides and polynucleotides useful for diagnosing,  
 PT preventing and treating cardiovascular disease, neurodegenerative,  
 PT hyperproliferative disorders and autoimmune disorders  
 XX XX  
 XX PS Disclosure; SEQ ID 1076; 1037pp; English.  
 XX XX  
 CC The present invention describes substantially purified human proteins  
 CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1  
 CC in the specification). ABN15762 to ABN27252 encode the human ORFX  
 CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for  
 CC treating or preventing a pathology associated with an ORFX-associated  
 CC disorder in humans, and in the manufacture of a medicament for treating a  
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide  
 CC sequences can be used in gene therapy. ORFX sequences can be used in the  
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,  
 CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,  
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ  
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic  
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester  
 CC storage disease, various immune deficiencies and disorders, infectious  
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid  
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host  
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also  
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,  
 CC bone degenerative disorders, or periodontal disease, and for gut  
 CC protection or regeneration and treatment of lung or liver fibrosis,  
 CC reperfusion injury in various tissues and conditions resulting from  
 CC systemic cytokine damage.  
 CC N.B. The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX XX  
 XX SQ Sequence 127 AA;  
 XX XX  
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 Best Local Similarity 100.0%; Pred. No. 0.0069;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 233 ANAALYLASDE 243

Db 99 ANAALYLASDE 109

Search completed: October 23, 2003, 13:02:43  
 Job time : 117 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 23, 2003, 13:00:45 ; Search time 29 Seconds  
(without alignments)  
398.306 Million cell updates/sec

Title: US-09-673-918A-2

Perfect score: 273

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Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued\_Patents\_AA.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	8	2.9	262	4	US-09-328-352-5742
4	8	2.9	267	4	US-09-252-991A-19626
5	8	2.9	290	4	US-09-134-001C-4339
6	8	2.9	295	3	US-09-026-482B-2
7	8	2.9	323	2	US-08-580-545B-2
8	8	2.9	323	3	US-09-262-653A-2
9	7	2.6	87	4	US-09-328-352-4279
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11	7	2.6	175	4	US-09-252-991A-18834
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13	7	2.6	261	3	US-08-815-225-2
14	7	2.6	261	3	US-08-815-225-3
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18	7	2.6	295	4	US-09-481-277-5
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25	7	2.6	401	4	US-09-252-991A-19274
26	7	2.6	429	3	US-09-293-395-3
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30	7	2.6	439	3	US-09-293-395-15	Sequence 15, Appl
31	7	2.6	439	3	US-09-668-648-15	Sequence 15, Appl
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34	7	2.6	481	3	US-09-330-095-1	Sequence 1, Appli
35	7	2.6	496	4	US-09-079-955-2	Sequence 2, Appli
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43	6	2.2	20	3	US-08-467-023-28	Sequence 28, Appl
44	6	2.2	30	4	US-09-570-921-114	Sequence 114, App
45	6	2.2	31	2	US-08-637-759B-454	Sequence 454, App
46	6	2.2	31	2	US-08-846-762-60	Sequence 60, Appl
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48	6	2.2	31	4	US-09-201-945-454	Sequence 454, App
49	6	2.2	47	4	US-09-690-454-58	Sequence 58, Appl
50	6	2.2	48	4	US-09-369-247-138	Sequence 138, App
51	6	2.2	50	3	US-08-467-023-66	Sequence 66, Appl
52	6	2.2	51	4	US-09-449-285A-21	Sequence 21, Appl
53	6	2.2	60	3	US-08-467-023-61	Sequence 61, Appl
54	6	2.2	69	4	US-09-252-991A-19836	Sequence 19836, A
55	6	2.2	71	4	US-09-328-352-4148	Sequence 4148, Ap
56	6	2.2	90	2	US-08-630-822A-66	Sequence 66, Appl
57	6	2.2	90	2	US-09-005-069-66	Sequence 66, Appl
58	6	2.2	90	4	US-09-171-156A-25	Sequence 25, Appl
59	6	2.2	90	4	US-09-004-730A-25	Sequence 25, Appl
60	6	2.2	90	4	US-08-981-799A-25	Sequence 25, Appl
61	6	2.2	90	4	US-09-107-532A-4618	Sequence 4618, Ap
62	6	2.2	103	4	US-09-134-001C-3894	Sequence 3894, Ap
63	6	2.2	109	4	US-09-087-031B-19	Sequence 19, Appl
64	6	2.2	111	3	US-08-961-083-180	Sequence 180, App
65	6	2.2	111	4	US-09-252-991A-17376	Sequence 17376, A
66	6	2.2	111	4	US-09-536-784-180	Sequence 180, App
67	6	2.2	114	4	US-09-252-991A-24819	Sequence 24819, A
68	6	2.2	118	4	US-09-252-991A-18229	Sequence 18229, A
69	6	2.2	119	1	US-08-053-171-12	Sequence 12, Appl
70	6	2.2	119	1	US-08-053-171-13	Sequence 13, Appl
71	6	2.2	119	1	US-08-053-171-14	Sequence 14, Appl
72	6	2.2	119	1	US-08-053-171-17	Sequence 17, Appl
73	6	2.2	119	3	US-08-815-190A-13	Sequence 13, Appl
74	6	2.2	123	1	US-08-256-261-10	Sequence 10, Appl
75	6	2.2	123	3	US-08-852-299-10	Sequence 10, Appl
76	6	2.2	126	1	US-08-075-545-2	Sequence 2, Appli
77	6	2.2	127	1	US-08-256-261-8	Sequence 8, Appli
78	6	2.2	127	3	US-08-852-299-8	Sequence 8, Appli
79	6	2.2	128	2	US-08-799-464A-26	Sequence 26, Appl
80	6	2.2	128	4	US-09-331-524-1	Sequence 1, Appli
81	6	2.2	128	5	PCT-US95-09927-26	Sequence 26, Appl
82	6	2.2	128	5	PCT-US95-10904-26	Sequence 26, Appl
83	6	2.2	131	2	US-08-477-451-30	Sequence 30, Appl
84	6	2.2	136	1	US-08-371-505-2	Sequence 2, Appli
85	6	2.2	136	2	US-08-784-971-5	Sequence 5, Appli
86	6	2.2	136	4	US-09-020-018-10	Sequence 10, Appl
87	6	2.2	136	4	US-09-252-991A-21678	Sequence 21678, A
88	6	2.2	137	1	US-08-256-261-2	Sequence 2, Appli
89	6	2.2	137	1	US-08-256-261-4	Sequence 4, Appli
90	6	2.2	137	1	US-08-256-261-6	Sequence 6, Appli
91	6	2.2	137	1	US-08-256-261-12	Sequence 12, Appl
92	6	2.2	137	1	US-08-256-261-14	Sequence 14, Appl
93	6	2.2	137	2	US-08-630-822A-64	Sequence 64, Appl
94	6	2.2	137	2	US-09-005-069-64	Sequence 64, Appl
95	6	2.2	137	3	US-08-852-299-2	Sequence 2, Appli
96	6	2.2	137	3	US-08-852-299-4	Sequence 4, Appli
97	6	2.2	137	3	US-08-852-299-6	Sequence 6, Appl
98	6	2.2	137	3	US-08-852-299-12	Sequence 12, Appl
99	6	2.2	137	3	US-08-852-299-14	Sequence 14, Appl
100	6	2.2	137	4	US-09-171-156A-23	Sequence 23, Appl

101	6	2.2	137	4	US-09-004-730A-23	Sequence 23, Appl	174	6	2.2	222	4	US-09-940-037A-2	Sequence 2, Appl
102	6	2.2	137	4	US-08-981-799A-23	Sequence 23, Appl	175	6	2.2	232	4	US-09-252-991A-28482	Sequence 28482, A
103	6	2.2	138	1	US-08-053-171-7	Sequence 7, Appl	176	6	2.2	232	4	US-09-328-352-6415	Sequence 6415, Ap
104	6	2.2	138	1	US-08-053-171-11	Sequence 11, Appl	177	6	2.2	234	4	US-09-134-001C-4059	Sequence 4059, Ap
105	6	2.2	139	1	US-08-120-607A-11	Sequence 11, Appl	178	6	2.2	235	4	US-09-468-738A-23	Sequence 23, Appl
106	6	2.2	140	1	US-09-904-615-16	Sequence 16, Appl	179	6	2.2	236	4	US-09-940-019-23	Sequence 23, Appl
107	6	2.2	140	4	US-09-107-532A-4251	Sequence 4251, Ap	180	6	2.2	236	4	US-09-940-037A-23	Sequence 23, Appl
108	6	2.2	143	4	US-09-732-210-1561	Sequence 1561, Ap	181	6	2.2	236	4	US-09-198-452A-218	Sequence 218, App
109	6	2.2	145	4	US-09-732-210-1561	Sequence 1593, Ap	182	6	2.2	236	4	US-09-252-991A-18282	Sequence 18282, A
110	6	2.2	155	6	5338678-2	Patent No. 5338678	183	6	2.2	310	4	US-09-252-991A-23088	Sequence 23088, A
111	6	2.2	158	6	5338678-2	Patent No. 5338678	184	6	2.2	314	4	US-09-087-031E-4	Sequence 4, Appl
112	6	2.2	162	4	US-09-006-428A-4	Sequence 4, Appl	185	6	2.2	314	4	US-09-087-031E-3	Sequence 3, Appl
113	6	2.2	163	1	US-08-075-545-1	Sequence 1, Appl	186	6	2.2	314	4	US-09-252-991A-31368	Sequence 31368, A
114	6	2.2	163	1	US-08-258-261-17	Sequence 17, Appl	187	6	2.2	315	3	US-08-793-035-9	Sequence 9, Appl
115	6	2.2	163	3	US-08-852-298-17	Sequence 17, Appl	188	6	2.2	315	3	US-08-793-035-10	Sequence 10, Appl
116	6	2.2	164	3	US-08-728-416C-3	Sequence 3, Appl	189	6	2.2	318	3	US-08-729-594A-39	Sequence 39, Appl
117	6	2.2	164	3	US-08-728-416C-13	Sequence 13, Appl	190	6	2.2	318	4	US-09-937-991A-39	Sequence 39, Appl
118	6	2.2	164	4	US-09-433-353-3	Sequence 3, Appl	191	6	2.2	337	4	US-09-252-991A-18869	Sequence 18869, A
119	6	2.2	164	4	US-09-433-353-13	Sequence 13, Appl	192	6	2.2	338	4	US-09-252-991A-31963	Sequence 31963, A
120	6	2.2	164	4	US-09-433-353-21	Sequence 21, Appl	193	6	2.2	339	4	US-09-107-532A-7038	Sequence 7038, Ap
121	6	2.2	171	4	US-09-252-991A-27423	Sequence 27423, A	194	6	2.2	332	4	US-09-830-217-20	Sequence 20, Appl
122	6	2.2	174	4	US-09-252-991A-32138	Sequence 32138, A	195	6	2.2	332	4	US-09-252-991A-21096	Sequence 21096, A
123	6	2.2	176	4	US-09-149-476-440	Sequence 440, App	196	6	2.2	332	4	US-09-252-991A-22834	Sequence 22834, A
124	6	2.2	182	4	US-09-252-991A-17529	Sequence 17529, A	197	6	2.2	332	4	US-09-252-991A-25234	Sequence 25234, A
125	6	2.2	188	4	US-09-252-991A-25186	Sequence 25186, A	198	6	2.2	332	4	US-09-252-991A-26386	Sequence 26386, A
126	6	2.2	202	4	US-09-252-991A-17114	Sequence 17114, A	199	6	2.2	336	3	US-08-855-910-6	Sequence 6, Appl
127	6	2.2	206	4	US-09-328-352-4683	Sequence 4683, Ap	200	6	2.2	337	1	US-08-440-856A-3	Sequence 3, Appl
128	6	2.2	214	4	US-09-252-991A-20677	Sequence 20677, A	201	6	2.2	338	1	US-08-218-686-2	Sequence 2, Appl
129	6	2.2	218	2	US-08-531-525-19	Sequence 19, Appl	202	6	2.2	338	2	US-08-441-857-10	Sequence 10, Appl
130	6	2.2	218	4	US-10-718-270A-19	Sequence 19, Appl	203	6	2.2	338	2	US-09-047-026A-2	Sequence 2, Appl
131	6	2.2	218	4	US-10-026-045-1	Sequence 1, Appl	204	6	2.2	338	3	US-08-460-242-2	Sequence 2, Appl
132	6	2.2	226	4	US-09-252-991A-30546	Sequence 30546, A	205	6	2.2	338	3	US-08-193-159-10	Sequence 10, Appl
133	6	2.2	229	4	US-09-252-991A-29751	Sequence 29751, A	206	6	2.2	339	4	US-09-252-991A-26600	Sequence 26600, A
134	6	2.2	230	4	US-09-252-991A-22090	Sequence 22090, A	207	6	2.2	341	4	US-09-369-247-132	Sequence 132, App
135	6	2.2	232	4	US-09-328-352-8025	Sequence 8025, Ap	208	6	2.2	342	4	US-09-415-277C-8	Sequence 8, Appl
136	6	2.2	236	4	US-09-252-991A-31916	Sequence 31916, A	209	6	2.2	345	1	US-07-954-840A-8	Sequence 8, Appl
137	6	2.2	239	4	US-09-252-991A-26390	Sequence 26390, A	210	6	2.2	345	1	US-07-954-840A-10	Sequence 10, Appl
138	6	2.2	241	4	US-08-178-257-19	Sequence 19, Appl	211	6	2.2	345	1	US-07-954-840A-12	Sequence 12, Appl
139	6	2.2	244	1	US-08-375-962B-13	Sequence 13, Appl	212	6	2.2	345	1	US-07-954-840A-14	Sequence 14, Appl
140	6	2.2	244	3	US-08-562-114B-13	Sequence 13, Appl	213	6	2.2	345	1	US-07-954-840A-16	Sequence 16, Appl
141	6	2.2	244	3	US-08-729-594A-13	Sequence 13, Appl	214	6	2.2	345	1	US-07-954-840A-18	Sequence 18, Appl
142	6	2.2	244	4	US-09-937-991A-13	Sequence 13, Appl	215	6	2.2	345	1	US-07-954-840A-20	Sequence 20, Appl
143	6	2.2	246	4	US-09-804-655-13	Sequence 13, Appl	216	6	2.2	345	1	US-07-954-840A-22	Sequence 22, Appl
144	6	2.2	251	3	US-08-822-322-9	Sequence 9, Appl	217	6	2.2	345	1	US-07-954-840A-24	Sequence 24, Appl
145	6	2.2	251	3	US-09-466-109-9	Sequence 9, Appl	218	6	2.2	345	1	US-07-954-840A-26	Sequence 26, Appl
146	6	2.2	251	4	US-09-198-452A-309	Sequence 309, App	219	6	2.2	347	1	US-07-637-870-5	Sequence 5, Appl
147	6	2.2	259	4	US-09-252-991A-28945	Sequence 28945, A	220	6	2.2	347	1	US-07-954-840A-2	Sequence 2, Appl
148	6	2.2	260	3	US-08-729-416C-21	Sequence 21, Appl	221	6	2.2	347	1	US-07-954-840A-4	Sequence 4, Appl
149	6	2.2	260	3	US-08-729-416C-22	Sequence 22, Appl	222	6	2.2	347	1	US-07-954-840A-6	Sequence 6, Appl
150	6	2.2	261	4	US-09-252-991A-17349	Sequence 17349, A	223	6	2.2	347	1	US-07-954-840A-28	Sequence 28, Appl
151	6	2.2	261	4	US-09-252-991A-28346	Sequence 28346, A	224	6	2.2	347	1	US-07-954-840A-29	Sequence 29, Appl
152	6	2.2	263	6	5229279-4	Patent No. 5229279	225	6	2.2	347	1	US-07-640-476-10	Sequence 10, Appl
153	6	2.2	267	4	US-09-328-352-6630	Sequence 6630, Ap	226	6	2.2	347	1	US-09-415-277C-11	Sequence 11, Appl
154	6	2.2	272	4	US-09-134-001C-2864	Sequence 2864, Ap	227	6	2.2	347	4	US-07-637-399-8	Sequence 8, Appl
155	6	2.2	272	4	US-09-328-352-7904	Sequence 7904, Ap	228	6	2.2	348	1	US-08-112-703-8	Sequence 8, Appl
156	6	2.2	273	1	US-08-137-175A-5	Sequence 5, Appl	229	6	2.2	348	4	US-09-415-277C-14	Sequence 14, Appl
157	6	2.2	273	3	US-09-196-293-13	Sequence 13, Appl	230	6	2.2	348	4	US-09-328-352-5513	Sequence 5513, Ap
158	6	2.2	273	3	US-08-209-603E-13	Sequence 13, Appl	231	6	2.2	349	4	US-09-134-001C-4884	Sequence 4884, Ap
159	6	2.2	273	3	US-08-235-836C-11	Sequence 11, Appl	232	6	2.2	349	4	US-09-300-971A-9	Sequence 9, Appl
160	6	2.2	273	3	US-08-235-836C-13	Sequence 13, Appl	233	6	2.2	349	4	US-09-328-352-5364	Sequence 5364, Ap
161	6	2.2	273	3	US-08-235-836C-89	Sequence 89, Appl	234	6	2.2	354	1	US-08-753-233-2	Sequence 2, Appl
162	6	2.2	273	3	US-08-235-836C-140	Sequence 140, App	235	6	2.2	354	2	US-08-984-246-2	Sequence 2, Appl
163	6	2.2	273	3	US-08-235-836C-142	Sequence 142, App	236	6	2.2	354	2	US-09-149-674-2	Sequence 2, Appl
164	6	2.2	273	3	US-08-235-836C-144	Sequence 144, App	237	6	2.2	354	2	US-09-580-929-5	Sequence 5, Appl
165	6	2.2	273	6	5512669-13	Patent No. 5512669	238	6	2.2	355	4	US-09-252-991A-19932	Sequence 19932, A
166	6	2.2	275	4	US-09-252-991A-27808	Sequence 27808, A	239	6	2.2	356	4	US-08-467-021-95	Sequence 95, Appl
167	6	2.2	286	4	US-09-328-352-7008	Sequence 7001, Ap	240	6	2.2	357	3	US-09-025-580-24	Sequence 24, Appl
168	6	2.2	288	4	US-09-216-393B-341	Sequence 341, App	241	6	2.2	357	4	US-09-025-580-24	Sequence 24, Appl
169	6	2.2	288	4	US-09-216-393B-341	Sequence 341, App	242	6	2.2	357	4	US-09-457-040B-13	Sequence 13, Appl
170	6	2.2	291	4	US-09-107-532A-7234	Sequence 7234, App	243	6	2.2	358	4	US-09-252-991A-56164	Sequence 56164, A
171	6	2.2	292	4	US-09-468-738A-2	Sequence 2, Appl	244	6	2.2	359	4	US-09-107-532A-51852	Sequence 51852, A
172	6	2.2	292	4	US-09-468-738A-2	Sequence 2, Appl	245	6	2.2	359	4	US-09-107-532A-5270	Sequence 5270, Ap
173	6	2.2	292	4	US-09-468-738A-2	Sequence 2, Appl	246	6	2.2	359	4	US-09-107-532A-5270	Sequence 5270, Ap



247	6	2.2	370	3	US-08-467-023-97	Sequence 97, Appl	320	6	2.2	467	3	US-09-046-736-2	Sequence 2, Appl
248	6	2.2	372	1	US-08-753-233-3	Sequence 3, Appl	321	6	2.2	471	4	US-09-328-532-5408	Sequence 5408, Ap
249	6	2.2	372	2	US-08-984-246-3	Sequence 3, Appl	322	6	2.2	471	4	US-09-107-332A-4629	Sequence 4629, Ap
250	6	2.2	372	2	US-09-149-674-3	Sequence 3, Appl	323	6	2.2	472	4	US-09-252-991A-26992	Sequence 26992, A
251	6	2.2	372	2	US-09-252-991A-29108	Sequence 29108, A	324	6	2.2	474	3	US-08-729-416C-1	Sequence 1, Appl
252	6	2.2	373	4	US-09-574-141A-57	Sequence 57, Appl	325	6	2.2	474	3	US-08-729-416C-11	Sequence 11, Appl
253	6	2.2	374	3	US-08-467-023-2	Sequence 2, Appl	326	6	2.2	474	3	US-08-807-342B-2	Sequence 2, Appl
254	6	2.2	374	3	US-09-046-736-4	Sequence 4, Appl	327	6	2.2	474	4	US-09-433-353-1	Sequence 1, Appl
255	6	2.2	377	3	US-09-352-990-28	Sequence 28, Appl	328	6	2.2	474	4	US-09-433-353-11	Sequence 11, Appl
256	6	2.2	385	4	US-09-570-778A-12	Sequence 12, Appl	329	6	2.2	474	4	US-09-252-991A-29269	Sequence 29269, A
257	6	2.2	385	4	US-09-991-138-12	Sequence 12, Appl	330	6	2.2	476	3	US-09-233-989-2	Sequence 2, Appl
258	6	2.2	386	4	US-09-383-318A-2	Sequence 2, Appl	331	6	2.2	476	3	US-09-233-989-3	Sequence 3, Appl
259	6	2.2	387	1	US-07-637-870-3	Sequence 3, Appl	332	6	2.2	476	3	US-09-233-989-6	Sequence 6, Appl
260	6	2.2	387	1	US-07-637-399-9	Sequence 9, Appl	333	6	2.2	477	4	US-09-252-991A-27516	Sequence 27516, A
261	6	2.2	387	1	US-07-640-476-12	Sequence 12, Appl	334	6	2.2	479	4	US-09-252-991A-25982	Sequence 25982, A
262	6	2.2	387	1	US-08-112-703-9	Sequence 9, Appl	335	6	2.2	479	4	US-09-328-352-4361	Sequence 4361, Ap
263	6	2.2	388	4	US-09-107-532A-5369	Sequence 5369, Ap	336	6	2.2	483	3	US-09-108-020-16	Sequence 16, Appl
264	6	2.2	393	1	US-08-029-404-2	Sequence 2, Appl	337	6	2.2	483	4	US-09-252-991A-29267	Sequence 29267, A
265	6	2.2	393	3	US-08-459-953A-2	Sequence 2, Appl	338	6	2.2	485	2	US-08-477-451-22	Sequence 22, Appl
266	6	2.2	393	4	US-09-331-924-8	Sequence 8, Appl	339	6	2.2	489	4	US-09-328-352-5088	Sequence 5088, Ap
267	6	2.2	394	2	US-09-393-212-2	Sequence 2, Appl	340	6	2.2	490	4	US-09-252-991A-24949	Sequence 24949, A
268	6	2.2	394	2	US-08-555-568B-17	Sequence 17, Appl	341	6	2.2	495	3	US-09-079-415-4	Sequence 4, Appl
269	6	2.2	394	3	US-08-519-223-17	Sequence 17, Appl	342	6	2.2	497	4	US-09-352-991A-22660	Sequence 22660, A
270	6	2.2	402	1	US-08-553-703A-1	Sequence 1, Appl	343	6	2.2	499	2	US-07-952-853-6	Sequence 6, Appl
271	6	2.2	402	1	US-08-553-703A-4	Sequence 4, Appl	344	6	2.2	499	2	US-08-914-848-6	Sequence 6, Appl
272	6	2.2	402	2	US-09-006-021-1	Sequence 1, Appl	345	6	2.2	500	1	US-07-755-573C-8	Sequence 8, Appl
273	6	2.2	402	2	US-09-006-021-4	Sequence 4, Appl	346	6	2.2	500	1	US-09-519-878-2	Sequence 2, Appl
274	6	2.2	404	3	US-08-459-953A-7	Sequence 7, Appl	347	6	2.2	511	3	US-08-931-952-4	Sequence 4, Appl
275	6	2.2	404	4	US-08-393-212-7	Sequence 7, Appl	348	6	2.2	511	3	US-08-272-247-4	Sequence 4, Appl
276	6	2.2	406	4	US-09-252-991A-20630	Sequence 20630, A	349	6	2.2	511	5	PCT-US95-08560-4	Sequence 4, Appl
277	6	2.2	414	3	US-09-067-626-4	Sequence 4, Appl	350	6	2.2	515	4	US-09-252-991A-27942	Sequence 27942, A
278	6	2.2	414	4	US-09-252-991A-21108	Sequence 21108, A	351	6	2.2	515	4	US-09-107-532A-6214	Sequence 6214, Ap
279	6	2.2	414	4	US-09-107-532A-7057	Sequence 7057, Ap	352	6	2.2	516	1	US-08-356-340-4	Sequence 4, Appl
280	6	2.2	417	1	US-08-553-703A-2	Sequence 2, Appl	353	6	2.2	516	2	US-08-786-555-4	Sequence 4, Appl
281	6	2.2	417	2	US-09-006-021-2	Sequence 2, Appl	354	6	2.2	521	4	US-09-352-991A-27321	Sequence 27321, A
282	6	2.2	417	4	US-09-328-352-6981	Sequence 6981, Ap	355	6	2.2	526	4	US-09-252-991A-20533	Sequence 20533, A
283	6	2.2	419	1	US-08-553-703A-3	Sequence 3, Appl	356	6	2.2	533	3	US-09-350-268-3	Sequence 3, Appl
284	6	2.2	419	2	US-09-006-021-3	Sequence 3, Appl	357	6	2.2	533	4	US-09-558-679-3	Sequence 3, Appl
285	6	2.2	422	4	US-09-252-991A-32607	Sequence 32607, A	358	6	2.2	533	4	US-09-347-650-17	Sequence 17, Appl
286	6	2.2	423	2	US-08-715-554-2	Sequence 2, Appl	359	6	2.2	534	3	US-09-124-541-1	Sequence 1, Appl
287	6	2.2	423	2	US-08-583-118-2	Sequence 2, Appl	360	6	2.2	535	4	US-09-352-991A-24728	Sequence 24728, A
288	6	2.2	425	4	US-09-252-991A-19692	Sequence 19692, A	361	6	2.2	545	4	US-08-976-063B-10	Sequence 10, Appl
289	6	2.2	432	4	US-09-443-041A-20	Sequence 20, Appl	362	6	2.2	558	4	US-09-252-991A-26115	Sequence 26115, A
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291	6	2.2	435	1	US-08-111-939-14	Sequence 14, Appl	364	6	2.2	569	4	US-09-252-991A-29263	Sequence 29263, A
292	6	2.2	435	1	US-08-111-939-15	Sequence 15, Appl	365	6	2.2	572	4	US-09-252-991A-17898	Sequence 17898, A
293	6	2.2	435	1	US-08-111-939-16	Sequence 16, Appl	366	6	2.2	583	3	US-09-272-414-2	Sequence 2, Appl
294	6	2.2	435	1	US-08-452-262-2	Sequence 2, Appl	367	6	2.2	585	2	US-08-453-848-11	Sequence 11, Appl
295	6	2.2	435	1	US-08-734-550-2	Sequence 2, Appl	368	6	2.2	585	3	US-09-169-027-11	Sequence 11, Appl
296	6	2.2	435	5	PCT-US96-07528-2	Sequence 2, Appl	369	6	2.2	592	2	US-08-453-848-19	Sequence 19, Appl
297	6	2.2	437	4	US-09-252-991A-18636	Sequence 18636, A	370	6	2.2	596	3	US-09-169-027-19	Sequence 19, Appl
298	6	2.2	438	3	US-08-486-099-93	Sequence 93, Appl	371	6	2.2	589	2	US-08-453-848-13	Sequence 13, Appl
299	6	2.2	438	3	US-08-360-107A-103	Sequence 103, App	372	6	2.2	589	3	US-09-169-027-13	Sequence 13, Appl
300	6	2.2	438	3	US-08-484-223B-93	Sequence 93, Appl	373	6	2.2	589	4	US-09-740-041-2	Sequence 2, Appl
301	6	2.2	438	3	US-08-919-597-93	Sequence 93, Appl	374	6	2.2	592	3	US-08-453-848-17	Sequence 17, Appl
302	6	2.2	438	3	US-08-475-668A-93	Sequence 93, Appl	375	6	2.2	592	3	US-09-169-027-17	Sequence 17, Appl
303	6	2.2	438	3	US-08-485-551A-93	Sequence 93, Appl	376	6	2.2	594	3	US-08-729-416C-7	Sequence 7, Appl
304	6	2.2	438	3	US-08-471-913A-93	Sequence 93, Appl	377	6	2.2	594	3	US-08-729-416C-17	Sequence 17, Appl
305	6	2.2	438	3	US-08-485-264A-93	Sequence 93, Appl	378	6	2.2	594	4	US-09-433-353-7	Sequence 7, Appl
306	6	2.2	438	4	US-08-474-349A-93	Sequence 93, Appl	379	6	2.2	594	4	US-09-433-353-17	Sequence 17, Appl
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309	6	2.2	438	4	US-08-485-546A-93	Sequence 93, Appl	382	6	2.2	607	4	US-09-568-102-9	Sequence 9, Appl
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311	6	2.2	441	4	US-09-252-991A-20573	Sequence 20573, A	384	6	2.2	607	4	US-09-568-486-9	Sequence 9, Appl
312	6	2.2	441	4	US-09-328-352-5426	Sequence 5426, Ap	385	6	2.2	607	4	US-09-568-486-9	Sequence 9, Appl
313	6	2.2	441	4	US-09-328-352-6745	Sequence 6745, Ap	386	6	2.2	607	4	US-09-568-472-9	Sequence 9, Appl
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317	6	2.2	457	4	US-09-252-991A-20955	Sequence 20955, A	390	6	2.2	619	5	PCT-US93-03027-6	Sequence 6, Appl
318	6	2.2	462	3	US-09-238-796-2	Sequence 2, Appl	391	6	2.2	628	4	US-09-252-991A-22131	Sequence 22131, A
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429	6	2.2	809	4	US-09-252-991A-29280	Sequence 29280, A	502	6	2.2	2647	2	US-08-779-113-8	Sequence 8, Appli
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435	6	2.2	833	4	US-09-229-059-4	Sequence 4, Appli	508	6	2.2	3170	4	US-09-603-207-4	Sequence 4, Appli
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450	6	2.2	951	4	US-09-252-991A-19440	Sequence 19440, A	523	6	2.2	4928	3	US-09-370-700-5	Sequence 5, Appli
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453	6	2.2	972	3	US-08-335-844A-23	Sequence 23, Appli	526	6	2.2	6095	3	US-09-144-085-2	Sequence 2, Appli
454	6	2.2	972	4	US-09-129-366-23	Sequence 23, Appli	527	5	1.8	7	4	US-09-374-454-16	Sequence 16, Appli
455	6	2.2	983	2	US-08-164-292B-26	Sequence 26, Appli	528	5	1.8	8	4	US-08-635-886C-143	Sequence 143, Appli
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457	6	2.2	983	3	US-08-815-927-26	Sequence 26, Appli	530	5	1.8	9	4	US-09-492-543-61	Sequence 61, Appli
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465	6	2.2	1036	4	US-09-536-224-4	Sequence 4, Appli	538	5	1.8	9	4	US-09-510-751A-6	Sequence 6, Appli

539	5	1.8	9	4	US-09-344-040C-76	Sequence 76, Appl	612	5	1.8	20	4	US-09-161-939A-11	Sequence 11, Appl
540	5	1.8	10	2	US-08-276-967-8	Sequence 8, Appli	613	5	1.8	20	4	US-09-205-258-489	Sequence 489, App
541	5	1.8	10	3	US-08-996-338-16	Sequence 16, Appl	614	5	1.8	20	5	PCT-US95-02626-13	Sequence 13, Appl
542	5	1.8	10	4	US-09-556-972-16	Sequence 16, Appl	615	5	1.8	20	6	547657-6	Patent No. 547657
543	5	1.8	11	1	US-08-411-727-2	Sequence 2, Appli	616	5	1.8	21	2	US-08-480-190-235	Sequence 235, App
544	5	1.8	11	2	US-08-385-335A-5	Sequence 5, Appli	617	5	1.8	21	2	US-08-488-379-235	Sequence 235, App
545	5	1.8	11	3	US-09-206-059-22	Sequence 22, Appl	618	5	1.8	21	3	US-08-256-747C-37	Sequence 37, Appl
546	5	1.8	11	3	US-09-206-059-24	Sequence 24, Appl	619	5	1.8	21	3	US-08-834-130A-37	Sequence 37, Appl
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548	5	1.8	12	2	US-08-637-759B-97	Sequence 97, Appl	621	5	1.8	21	4	US-08-924-629C-13	Sequence 13, Appl
549	5	1.8	12	3	US-08-871-355A-97	Sequence 97, Appl	622	5	1.8	21	4	US-09-139-600-14	Sequence 14, Appl
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551	5	1.8	12	4	US-09-201-945-97	Sequence 97, Appl	624	5	1.8	21	4	US-08-475-399A-235	Sequence 235, App
552	5	1.8	13	2	US-08-637-759B-193	Sequence 193, App	625	5	1.8	21	5	PCT-US93-07545-235	Sequence 235, App
553	5	1.8	13	3	US-08-871-355A-193	Sequence 193, App	626	5	1.8	22	1	US-08-460-874A-37	Sequence 37, Appl
554	5	1.8	13	3	US-08-928-383B-7	Sequence 7, Appli	627	5	1.8	22	2	US-08-388-883B-37	Sequence 37, Appl
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557	5	1.8	14	2	US-08-937-102-25	Sequence 25, Appl	630	5	1.8	23	2	US-08-480-190-157	Sequence 157, App
558	5	1.8	14	3	US/08/622	INFORMATION FOR	631	5	1.8	23	2	US-08-480-190-174	Sequence 174, App
559	5	1.8	14	3	US-08-960-190A-29	Sequence 29, Appl	632	5	1.8	23	2	US-08-488-379-157	Sequence 157, App
560	5	1.8	14	4	US-09-165-922A-2	Sequence 2, Appli	633	5	1.8	23	2	US-08-488-379-274	Sequence 274, App
561	5	1.8	15	1	US-07-907-190-4	Sequence 4, Appli	634	5	1.8	23	4	US-08-475-399A-157	Sequence 157, App
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563	5	1.8	15	1	US-08-442-063A-21	Sequence 21, Appl	636	5	1.8	23	4	US-09-281-495-1	Sequence 1, Appli
564	5	1.8	15	2	US-08-695-412B-1	Sequence 1, Appli	637	5	1.8	23	5	PCT-US93-07545-18	Sequence 18, Appl
565	5	1.8	15	2	US-08-683-262B-70	Sequence 70, Appl	638	5	1.8	23	5	US-09-509-593-18	Sequence 18, Appl
566	5	1.8	15	2	US-08-937-102-23	Sequence 23, Appl	639	5	1.8	24	1	US-08-141-324-21	Sequence 21, Appl
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569	5	1.8	15	3	US-08-874-197-5	Sequence 5, Appli	642	5	1.8	24	2	US-08-679-405-5	Sequence 5, Appli
570	5	1.8	15	3	US-08-874-197-9	Sequence 9, Appli	643	5	1.8	24	2	US-08-842-799-5	Sequence 5, Appli
571	5	1.8	15	3	US-09-361-707-70	Sequence 70, Appl	644	5	1.8	24	3	US-08-855-958-6	Sequence 6, Appli
572	5	1.8	15	4	US-08-648-182-5	Sequence 5, Appli	645	5	1.8	24	5	PCT-US96-11459-5	Sequence 5, Appli
573	5	1.8	15	4	US-08-648-182-9	Sequence 9, Appli	646	5	1.8	25	1	US-08-614-935-69	Sequence 69, Appl
574	5	1.8	15	4	US-09-165-922A-1	Sequence 1, Appli	647	5	1.8	25	2	US-08-902-516-4	Sequence 4, Appli
575	5	1.8	15	4	US-09-490-702B-20	Sequence 20, Appl	648	5	1.8	25	3	US-09-130-287-69	Sequence 69, Appl
576	5	1.8	16	1	US-08-164-839-55	Sequence 55, Appl	649	5	1.8	25	4	US-09-847-185-4	Sequence 4, Appli
577	5	1.8	16	1	US-08-218-025A-12	Sequence 12, Appl	650	5	1.8	26	4	US-09-509-593-17	Sequence 17, Appl
578	5	1.8	16	1	US-08-583-799-55	Sequence 55, Appl	651	5	1.8	26	4	US-09-120-365-33	Sequence 33, Appl
579	5	1.8	16	2	US-08-385-335A-6	Sequence 6, Appli	652	5	1.8	27	3	US-09-515-039-33	Sequence 33, Appl
580	5	1.8	16	3	US-09-434-774-13	Sequence 13, Appl	653	5	1.8	27	3	US-09-509-593-16	Sequence 16, Appl
581	5	1.8	16	4	US-09-574-749B-58	Sequence 58, Appl	654	5	1.8	28	1	US-08-276-213-4	Sequence 4, Appli
582	5	1.8	17	2	US-08-480-190-236	Sequence 236, App	655	5	1.8	28	1	US-07-977-630-46	Sequence 46, Appl
583	5	1.8	17	2	US-08-637-763B-2	Sequence 2, Appli	656	5	1.8	28	1	US-08-440-391-2	Sequence 2, Appli
584	5	1.8	17	2	US-08-488-379-236	Sequence 236, App	657	5	1.8	28	1	US-08-440-391-18	Sequence 18, Appl
585	5	1.8	17	3	US-09-170-354-2	Sequence 2, Appli	658	5	1.8	28	2	US-08-908-597A-2	Sequence 2, Appli
586	5	1.8	17	4	US-08-475-399A-236	Sequence 236, App	659	5	1.8	28	2	US-08-908-597A-18	Sequence 18, Appl
587	5	1.8	17	5	PCT-US93-07545-236	Sequence 236, App	660	5	1.8	28	3	US-09-236-385A-2	Sequence 2, Appli
588	5	1.8	18	1	US-08-391-000-1	Sequence 1, Appli	661	5	1.8	28	3	US-09-236-385A-18	Sequence 18, Appl
589	5	1.8	18	2	US-08-741-931-1	Sequence 1, Appli	662	5	1.8	28	5	PCT-US96-06122-2	Sequence 2, Appli
590	5	1.8	18	2	US-08-923-274-17	Sequence 17, Appl	663	5	1.8	28	5	PCT-US96-06122-18	Sequence 18, Appl
591	5	1.8	18	2	US-08-959-536-17	Sequence 17, Appl	664	5	1.8	29	2	US-08-846-762-56	Sequence 56, Appl
592	5	1.8	18	4	US-09-447-125B-27	Sequence 27, Appl	665	5	1.8	29	2	US-08-846-762-65	Sequence 65, Appl
593	5	1.8	18	4	US-09-552-802B-27	Sequence 27, Appl	666	5	1.8	30	3	US-08-467-023-260	Sequence 260, App
594	5	1.8	19	4	US-08-950-888-15	Sequence 15, Appl	667	5	1.8	30	3	US-09-425-638A-101	Sequence 101, App
595	5	1.8	20	1	US-07-777-715-4	Sequence 4, Appli	668	5	1.8	30	4	BARTHOLD-	Sequence 4, Appli
596	5	1.8	20	1	US-08-205-338A-13	Sequence 13, Appl	669	5	1.8	30	4	US-09-543-004-101	Sequence 101, App
597	5	1.8	20	1	US-07-908-253-5	Sequence 5, Appli	670	5	1.8	30	4	US-09-205-258-521	Sequence 521, App
598	5	1.8	20	1	US-08-218-025A-59	Sequence 49, Appl	671	5	1.8	31	3	US-09-045-632-73	Sequence 73, Appl
599	5	1.8	20	1	US-08-218-025A-40	Sequence 50, Appl	672	5	1.8	32	1	US-08-190-802A-180	Sequence 180, App
600	5	1.8	20	1	US-08-170-126-6	Sequence 6, Appli	673	5	1.8	32	1	US-08-190-802A-181	Sequence 181, App
601	5	1.8	20	1	US-08-321-071A-19	Sequence 19, Appl	674	5	1.8	32	3	US-08-477-346-180	Sequence 180, App
602	5	1.8	20	1	US-08-306-116A-11	Sequence 11, Appl	675	5	1.8	32	3	US-08-477-346-181	Sequence 181, App
603	5	1.8	20	2	US-08-535-837-5	Sequence 5, Appli	676	5	1.8	32	4	US-08-473-089-180	Sequence 180, App
604	5	1.8	20	3	US-08-467-023-29	Sequence 29, Appl	677	5	1.8	32	4	US-08-473-089-181	Sequence 181, App
605	5	1.8	20	3	US-08-954-418-6	Sequence 6, Appli	678	5	1.8	32	4	US-08-487-072A-180	Sequence 180, App
606	5	1.8	20	3	US-08-602-999A-114	Sequence 114, App	679	5	1.8	32	4	US-08-487-072A-181	Sequence 181, App
607	5	1.8	20	4	US-09-439-313-494	Sequence 494, App	680	5	1.8	33	2	US-09-031-485-84	Sequence 84, Appl
608	5	1.8	20	4	US-09-304-799-2	Sequence 2, Appli	681	5	1.8	33	2	US-08-847-429A-84	Sequence 84, Appl
609	5	1.8	20	4	US-09-257-179-92	Sequence 92, Appl	682	5	1.8	33	2	US-08-640-847C-5	Sequence 5, Appli
610	5	1.8	20	4	US-09-500-124-114	Sequence 114, App	683	5	1.8	33	3	US-08-651-136C-30	Sequence 30, Appl
611	5	1.8	20	4	US-09-161-939A-10	Sequence 10, Appl	684	5	1.8	33	3	US-09-065-474-84	Sequence 84, Appl

685	5	1.8	33	4	US-09-557-034-84	Sequence 84, Appl	758	5	1.8	48	3	US-08-804-439A-105	Sequence 105, Appl
686	5	1.8	33	4	US-08-978-285-1	Sequence 1, Appl	759	5	1.8	48	3	US-09-004-406C-23	Sequence 23, Appl
687	5	1.8	33	4	US-09-229-911A-30	Sequence 30, Appl	760	5	1.8	48	3	US-09-042-071-26	Sequence 26, Appl
688	5	1.8	33	4	US-08-585-468-3	Sequence 3, Appl	761	5	1.8	48	3	US-09-461-325-143	Sequence 143, Appl
689	5	1.8	36	1	US-08-908-391-14	Sequence 14, Appl	762	5	1.8	48	4	US-09-205-258-1023	Sequence 1023, App
690	5	1.8	36	2	US-08-908-597A-14	Sequence 14, Appl	763	5	1.8	49	1	US-08-118-370-201	Sequence 201, App
691	5	1.8	36	3	US-09-236-385A-14	Sequence 14, Appl	764	5	1.8	49	1	US-08-262-037-65	Sequence 65, Appl
692	5	1.8	36	4	US-09-315-304B-1482	Sequence 1482, Ap	765	5	1.8	49	4	US-09-227-357-595	Sequence 595, App
693	5	1.8	36	4	US-09-288-143-130	Sequence 130, App	766	5	1.8	49	4	US-09-377-466B-27	Sequence 27, Appl
694	5	1.8	36	5	PCT-US96-06122-14	Sequence 14, Appl	767	5	1.8	49	4	PCT-US91-08528-201	Sequence 201, Appl
695	5	1.8	37	1	US-08-130-802A-169	Sequence 169, App	768	5	1.8	50	4	US-08-963-851-9	Sequence 9, Appl
696	5	1.8	37	1	US-08-130-802A-214	Sequence 214, App	769	5	1.8	51	2	US-08-322-825-29	Sequence 29, Appl
697	5	1.8	37	3	US-08-477-346-169	Sequence 169, App	770	5	1.8	51	2	US-08-466-361A-29	Sequence 29, Appl
698	5	1.8	37	3	US-08-477-346-214	Sequence 214, App	771	5	1.8	53	3	US-09-155-107-15	Sequence 15, Appl
699	5	1.8	37	4	US-08-473-089-169	Sequence 169, App	772	5	1.8	53	3	US-09-155-107-16	Sequence 16, Appl
700	5	1.8	37	4	US-08-473-089-214	Sequence 214, App	773	5	1.8	53	3	US-09-155-107-17	Sequence 17, Appl
701	5	1.8	37	4	US-08-487-072A-169	Sequence 169, App	774	5	1.8	53	3	US-09-155-107-18	Sequence 18, Appl
702	5	1.8	37	4	US-08-487-072A-214	Sequence 214, App	775	5	1.8	53	3	US-09-042-071-37	Sequence 37, Appl
703	5	1.8	38	1	US-08-176-500-70	Sequence 70, Appl	776	5	1.8	56	2	US-08-867-087B-29	Sequence 29, Appl
704	5	1.8	38	1	US-07-956-700B-41	Sequence 41, Appl	777	5	1.8	58	1	US-08-262-037-77	Sequence 77, Appl
705	5	1.8	38	1	US-07-956-700B-52	Sequence 52, Appl	778	5	1.8	58	1	US-08-274-366-2	Sequence 2, Appl
706	5	1.8	38	1	US-08-471-052A-70	Sequence 70, Appl	779	5	1.8	58	2	US-08-572-951-37	Sequence 37, Appl
707	5	1.8	38	1	US-08-262-037-55	Sequence 55, Appl	780	5	1.8	58	2	US-08-152-721B-19	Sequence 19, Appl
708	5	1.8	38	1	US-08-189-331-70	Sequence 70, Appl	781	5	1.8	58	3	US-08-735-491-5	Sequence 5, Appl
709	5	1.8	38	1	US-08-476-537-41	Sequence 41, Appl	782	5	1.8	58	3	US-08-941-445A-34	Sequence 34, Appl
710	5	1.8	38	1	US-08-476-537-52	Sequence 52, Appl	783	5	1.8	58	5	PCT-US95-07828-2	Sequence 2, Appl
711	5	1.8	38	1	US-08-485-607-41	Sequence 41, Appl	784	5	1.8	59	1	US-08-262-037-66	Sequence 66, Appl
712	5	1.8	38	1	US-08-485-607-52	Sequence 52, Appl	785	5	1.8	59	2	US-08-392-816-18	Sequence 18, Appl
713	5	1.8	38	2	US-08-471-939-70	Sequence 70, Appl	786	5	1.8	60	4	US-08-924-629C-74	Sequence 74, Appl
714	5	1.8	38	2	US-08-471-939-70	Sequence 70, Appl	787	5	1.8	60	4	US-09-702-705-799	Sequence 799, App
715	5	1.8	38	2	US-08-471-968-70	Sequence 70, Appl	788	5	1.8	60	4	US-09-702-705-799	Sequence 799, App
716	5	1.8	38	2	US-08-475-879-41	Sequence 41, Appl	789	5	1.8	60	4	US-09-702-705-799	Sequence 799, App
717	5	1.8	38	2	US-08-475-879-52	Sequence 52, Appl	790	5	1.8	61	4	US-09-702-705-799	Sequence 799, App
718	5	1.8	38	3	US-08-527-219-35	Sequence 35, Appl	791	5	1.8	61	4	US-09-702-705-799	Sequence 799, App
719	5	1.8	38	3	US-09-172-841-23	Sequence 23, Appl	792	5	1.8	63	2	US-08-338-530A-6	Sequence 6, Appl
720	5	1.8	38	4	US-09-433-043B-41	Sequence 41, Appl	793	5	1.8	63	3	US-09-061-026-16	Sequence 16, Appl
721	5	1.8	38	4	US-09-433-043B-52	Sequence 52, Appl	794	5	1.8	63	3	US-09-061-026-22	Sequence 22, Appl
722	5	1.8	38	4	US-09-433-043B-52	Sequence 52, Appl	795	5	1.8	63	3	US-09-466-138-16	Sequence 16, Appl
723	5	1.8	39	1	US-08-951-621-23	Sequence 23, Appl	796	5	1.8	63	3	US-09-466-138-22	Sequence 22, Appl
724	5	1.8	39	1	US-09-220-528-49	Sequence 49, Appl	797	5	1.8	63	3	US-09-267-384-6	Sequence 6, Appl
725	5	1.8	40	2	US-08-262-037-64	Sequence 64, Appl	798	5	1.8	63	4	US-09-134-001C-2886	Sequence 2886, Ap
726	5	1.8	40	2	US-08-807-332B-32	Sequence 32, Appl	799	5	1.8	63	4	US-09-706-770-6	Sequence 6, Appl
727	5	1.8	40	3	US-09-154-083-16	Sequence 16, Appl	800	5	1.8	64	4	US-09-134-001C-5429	Sequence 5429, Ap
728	5	1.8	41	3	US-09-177-249-57	Sequence 57, Appl	801	5	1.8	64	4	US-09-252-991A-17573	Sequence 17573, A
729	5	1.8	41	4	US-09-399-913-40	Sequence 40, Appl	802	5	1.8	64	4	US-09-252-991A-25618	Sequence 25618, A
730	5	1.8	41	4	US-09-298-731-40	Sequence 40, Appl	803	5	1.8	64	4	US-09-328-352-4697	Sequence 4697, Ap
731	5	1.8	42	1	US-08-377-687-39	Sequence 39, Appl	804	5	1.8	65	4	US-09-107-532A-4834	Sequence 4834, Ap
732	5	1.8	42	2	US-08-377-687-39	Sequence 39, Appl	805	5	1.8	65	4	US-08-981-392-36	Sequence 36, Appl
733	5	1.8	42	3	US-08-971-982-39	Sequence 39, Appl	806	5	1.8	65	4	US-09-107-532A-6375	Sequence 6375, Ap
734	5	1.8	43	3	US-09-188-930-175	Sequence 175, App	807	5	1.8	66	4	US-09-205-258-520	Sequence 520, App
735	5	1.8	43	3	US-09-188-930-318	Sequence 318, App	808	5	1.8	66	4	US-09-205-258-520	Sequence 520, App
736	5	1.8	43	4	US-08-675-499A-10	Sequence 10, Appl	809	5	1.8	67	1	US-08-203-806B-12	Sequence 12, Appl
737	5	1.8	43	4	US-09-312-283C-175	Sequence 175, App	810	5	1.8	67	3	US-08-243-575-4	Sequence 4, Appl
738	5	1.8	43	4	US-09-312-283C-318	Sequence 318, App	811	5	1.8	67	4	US-09-017-754A-12	Sequence 12, Appl
739	5	1.8	44	3	US-09-071-710-37	Sequence 37, Appl	812	5	1.8	67	4	US-09-134-001C-5270	Sequence 5270, Ap
740	5	1.8	44	3	US-09-525-397-37	Sequence 37, Appl	813	5	1.8	67	4	US-09-482-273-144	Sequence 144, App
741	5	1.8	45	3	US-09-018-635-37	Sequence 37, Appl	814	5	1.8	67	4	US-09-328-352-5686	Sequence 5686, Ap
742	5	1.8	45	3	US-09-018-635-39	Sequence 39, Appl	815	5	1.8	67	4	US-09-107-532A-6754	Sequence 6754, Ap
743	5	1.8	45	4	US-09-912-962-37	Sequence 37, Appl	816	5	1.8	68	1	US-08-262-037-67	Sequence 67, Appl
744	5	1.8	45	4	US-09-912-962-39	Sequence 39, Appl	817	5	1.8	68	1	US-08-466-033-148	Sequence 148, App
745	5	1.8	46	1	US-08-463-128-41	Sequence 41, Appl	818	5	1.8	68	2	US-08-444-733-148	Sequence 148, App
746	5	1.8	46	3	US-08-463-180-41	Sequence 41, Appl	819	5	1.8	68	2	US-08-461-361-148	Sequence 148, App
747	5	1.8	46	3	US-08-857-076-83	Sequence 83, Appl	820	5	1.8	68	2	US-08-485-910-148	Sequence 148, App
748	5	1.8	47	1	US-08-118-270-203	Sequence 203, Appl	821	5	1.8	68	2	US-09-134-001C-3029	Sequence 3029, Ap
749	5	1.8	47	1	US-08-443-063A-30	Sequence 30, Appl	822	5	1.8	68	4	US-09-134-001C-13	Sequence 13, Appl
750	5	1.8	47	1	US-08-443-063A-51	Sequence 51, Appl	823	5	1.8	69	4	US-09-134-001C-3193	Sequence 3193, Ap
751	5	1.8	47	1	US-08-443-063A-54	Sequence 54, Appl	824	5	1.8	69	4	US-09-134-001C-3406	Sequence 3406, Ap
752	5	1.8	47	4	US-08-469-260A-600	Sequence 600, App	825	5	1.8	69	4	US-09-732-210-1122	Sequence 1122, Ap
753	5	1.8	47	4	US-08-469-260A-600	Sequence 600, App	826	5	1.8	69	4	US-08-311-731A-215	Sequence 215, App
754	5	1.8	47	4	US-08-488-446-600	Sequence 600, App	827	5	1.8	69	4	US-08-858-207A-514	Sequence 514, App
755	5	1.8	47	4	US-08-488-446-600	Sequence 600, App	828	5	1.8	70	4	US-08-262-037-56	Sequence 56, Appl
756	5	1.8	47	5	PCT-US93-08528-203	Sequence 203, App	829	5	1.8	71	1	US-08-262-037-56	Sequence 56, Appl
757	5	1.8	48	1	US-07-835-860-1	Sequence 1, Appl	830	5	1.8	71	4	US-09-369-247-79	Sequence 79, Appl

831	5	1.8	72	3	US-09-383-586-38	Sequence 38, Appl	904	5	1.8	96	2	US-08-470-868A-35	Sequence 35, Appl
832	5	1.8	72	4	US-09-134-001C-3540	Sequence 3540, Ap	905	5	1.8	96	3	US-09-210-681A-35	Sequence 35, Appl
833	5	1.8	75	4	US-09-450-072-70	Sequence 70, Appl	906	5	1.8	96	3	US-08-946-719A-35	Sequence 35, Appl
834	5	1.8	75	4	US-09-351-348-70	Sequence 70, Appl	907	5	1.8	96	4	US-09-547-983-35	Sequence 35, Appl
835	5	1.8	76	1	US-08-848-252-4	Sequence 4, Appl	908	5	1.8	97	1	US-08-262-037-61	Sequence 61, Appl
836	5	1.8	76	4	US-09-020-846-39	Sequence 39, Appl	909	5	1.8	97	4	US-09-107-532A-6903	Sequence 6903, Ap
837	5	1.8	76	4	US-09-328-352-6085	Sequence 6085, Ap	910	5	1.8	97	4	US-09-107-532A-7243	Sequence 7243, Ap
838	5	1.8	77	1	US-08-262-037-68	Sequence 68, Appl	911	5	1.8	98	2	US-08-454-557C-30	Sequence 30, Appl
839	5	1.8	77	2	US-08-726-306A-32	Sequence 32, Appl	912	5	1.8	98	2	US-08-340-426D-30	Sequence 30, Appl
840	5	1.8	77	4	US-09-328-352-4275	Sequence 4275, Ap	913	5	1.8	98	2	US-08-450-673C-30	Sequence 30, Appl
841	5	1.8	77	4	US-09-328-352-5944	Sequence 5944, Ap	914	5	1.8	98	2	US-08-481-658B-50	Sequence 50, Appl
842	5	1.8	78	1	US-07-991-867B-4	Sequence 4, Appl	915	5	1.8	98	2	US-08-477-504A-50	Sequence 50, Appl
843	5	1.8	78	1	US-08-107-755A-4	Sequence 4, Appl	916	5	1.8	98	2	US-08-486-756A-50	Sequence 50, Appl
844	5	1.8	78	2	US-08-544-332-4	Sequence 4, Appl	917	5	1.8	98	2	US-08-485-62B-50	Sequence 50, Appl
845	5	1.8	78	4	US-09-370-861A-4	Sequence 4, Appl	918	5	1.8	98	3	US-08-487-077A-50	Sequence 50, Appl
846	5	1.8	78	4	US-09-107-532A-5823	Sequence 5823, Ap	919	5	1.8	98	3	US-08-485-863A-50	Sequence 50, Appl
847	5	1.8	78	4	US-09-107-532A-7263	Sequence 7263, Ap	920	5	1.8	98	3	US-08-485-049D-50	Sequence 50, Appl
848	5	1.8	79	1	US-08-665-220-68	Sequence 68, Appl	921	5	1.8	98	4	US-09-147-857-3	Sequence 3, Appl
849	5	1.8	79	2	US-09-174-060-5	Sequence 5, Appl	922	5	1.8	98	4	US-09-134-001C-4312	Sequence 4312, Ap
850	5	1.8	79	3	US-09-053-197A-15	Sequence 15, Appl	923	5	1.8	98	4	US-09-252-991A-23171	Sequence 23171, A
851	5	1.8	79	3	US-08-338-382-5	Sequence 5, Appl	924	5	1.8	98	5	PCT-US95-17111A-30	Sequence 30, Appl
852	5	1.8	79	3	US-09-291-692-68	Sequence 68, Appl	925	5	1.8	99	2	US-08-858-767-28	Sequence 28, Appl
853	5	1.8	79	4	US-09-085-761A-15	Sequence 15, Appl	926	5	1.8	99	2	US-08-863-028-28	Sequence 28, Appl
854	5	1.8	79	4	US-09-186-002-4	Sequence 4, Appl	927	5	1.8	99	4	US-09-370-838-95	Sequence 95, Appl
855	5	1.8	79	4	US-09-377-466B-26	Sequence 26, Appl	928	5	1.8	99	4	US-09-634-238-305	Sequence 305, App
856	5	1.8	79	4	US-09-252-991A-21406	Sequence 21406, A	929	5	1.8	99	4	US-09-252-991A-18340	Sequence 18340, A
857	5	1.8	79	4	US-09-107-532A-5614	Sequence 5614, Ap	930	5	1.8	100	4	US-09-397-787-18	Sequence 18, Appl
858	5	1.8	80	1	US-08-848-252-2	Sequence 2, Appl	931	5	1.8	100	4	US-09-198-452A-1076	Sequence 1076, Ap
859	5	1.8	81	4	US-08-252-991A-18646	Sequence 18646, A	932	5	1.8	100	4	US-09-886-319A-16	Sequence 16, Appl
860	5	1.8	81	4	US-09-198-452A-1027	Sequence 1027, Ap	933	5	1.8	101	1	US-08-220-401-5	Sequence 5, Appl
861	5	1.8	82	3	US-09-014-438-1	Sequence 1, Appl	934	5	1.8	101	2	US-08-437-362-5	Sequence 5, Appl
862	5	1.8	82	4	US-09-482-273-156	Sequence 156, App	935	5	1.8	101	3	US-09-374-135-6	Sequence 6, Appl
863	5	1.8	83	3	US-09-382-155-12	Sequence 12, Appl	936	5	1.8	101	4	US-09-599-160B-119	Sequence 119, App
864	5	1.8	83	3	US-09-074-044A-12	Sequence 12, Appl	937	5	1.8	101	4	US-09-107-532A-3974	Sequence 3974, Ap
865	5	1.8	83	4	US-08-198-452A-21	Sequence 21, Appl	938	5	1.8	102	4	US-09-732-210-1283	Sequence 1283, Ap
866	5	1.8	83	4	US-09-328-352-5531	Sequence 5531, Ap	939	5	1.8	103	4	US-08-924-629C-39	Sequence 39, Appl
867	5	1.8	84	4	US-09-107-532A-4957	Sequence 4957, Ap	940	5	1.8	103	4	US-09-107-532A-4967	Sequence 4967, Ap
868	5	1.8	84	3	US-09-107-532A-7177	Sequence 7177, Ap	941	5	1.8	105	2	US-08-241-853-11	Sequence 11, Appl
869	5	1.8	84	3	US-09-107-858-27	Sequence 27, Appl	942	5	1.8	105	2	US-08-850-917-11	Sequence 11, Appl
870	5	1.8	84	3	US-09-386-493-14	Sequence 14, Appl	943	5	1.8	105	4	US-09-025-769B-166	Sequence 166, App
871	5	1.8	84	4	US-08-439-313-571	Sequence 571, App	944	5	1.8	105	4	US-09-252-991A-27412	Sequence 27412, A
872	5	1.8	84	4	US-08-932-991A-19809	Sequence 19809, A	945	5	1.8	105	4	US-09-328-352-4390	Sequence 4390, Ap
873	5	1.8	84	4	US-09-328-352-5661	Sequence 5661, Ap	946	5	1.8	106	2	US-08-378-939-40	Sequence 40, Appl
874	5	1.8	85	4	US-09-134-001C-5110	Sequence 5110, Ap	947	5	1.8	106	2	US-08-378-939-42	Sequence 42, Appl
875	5	1.8	85	4	US-08-311-731A-323	Sequence 323, App	948	5	1.8	106	2	US-08-761-277A-49	Sequence 49, Appl
876	5	1.8	85	4	US-09-107-532A-3695	Sequence 3695, Ap	949	5	1.8	106	3	US-08-444-644-26	Sequence 26, Appl
877	5	1.8	86	3	US-08-905-223-429	Sequence 429, App	950	5	1.8	106	3	US-08-946-329A-76	Sequence 76, Appl
878	5	1.8	89	1	US-08-181-556-2	Sequence 2, Appl	951	5	1.8	106	4	US-08-232-246A-26	Sequence 26, Appl
879	5	1.8	89	4	US-08-686-878A-21	Sequence 21, Appl	952	5	1.8	106	4	US-08-936-165A-482	Sequence 482, App
880	5	1.8	89	4	US-09-175-928-21	Sequence 21, Appl	953	5	1.8	106	4	US-09-107-532A-5357	Sequence 5357, Ap
881	5	1.8	89	4	US-09-453-956-4	Sequence 4, Appl	954	5	1.8	107	1	US-07-893-929A-6	Sequence 6, Appl
882	5	1.8	89	4	US-08-252-991A-22408	Sequence 22408, A	955	5	1.8	107	1	US-08-422-101-8	Sequence 8, Appl
883	5	1.8	90	1	US-08-591-498-13	Sequence 13, Appl	956	5	1.8	107	1	US-08-422-091-8	Sequence 8, Appl
884	5	1.8	90	4	US-09-328-352-6160	Sequence 6160, Ap	957	5	1.8	107	2	US-08-422-092-8	Sequence 8, Appl
885	5	1.8	90	6	5218099-3	Patent No. 5218099	958	5	1.8	107	2	US-08-788-800-5	Sequence 5, Appl
886	5	1.8	91	4	US-09-424-311-4	Sequence 4, Appl	959	5	1.8	107	2	US-08-422-093-8	Sequence 8, Appl
887	5	1.8	91	4	US-08-983-502-22	Sequence 22, Appl	960	5	1.8	107	3	US-08-422-112-8	Sequence 8, Appl
888	5	1.8	91	4	US-08-983-502-34	Sequence 34, Appl	961	5	1.8	107	3	US-09-102-528-23	Sequence 23, Appl
889	5	1.8	91	4	US-09-516-747-22	Sequence 22, Appl	962	5	1.8	107	3	US-09-102-528-27	Sequence 27, Appl
890	5	1.8	91	4	US-09-516-747-34	Sequence 34, Appl	963	5	1.8	107	4	US-09-134-001C-2849	Sequence 2849, Ap
891	5	1.8	91	5	PCT-US96-10521-22	Sequence 22, Appl	964	5	1.8	107	4	US-09-301-593-20	Sequence 20, Appl
892	5	1.8	91	5	PCT-US96-10521-34	Sequence 34, Appl	965	5	1.8	107	4	US-09-461-325-484	Sequence 484, App
893	5	1.8	92	1	US-08-319-387-3	Sequence 3, Appl	966	5	1.8	107	5	PCT-US92-10344-6	Sequence 6, Appl
894	5	1.8	92	4	US-08-936-165A-313	Sequence 313, App	967	5	1.8	108	4	US-09-313-942-13	Sequence 13, Appl
895	5	1.8	92	4	US-09-370-838-211	Sequence 211, App	968	5	1.8	109	1	US-08-436-463-8	Sequence 8, Appl
896	5	1.8	93	4	US-09-312-283C-421	Sequence 421, App	969	5	1.8	109	1	US-08-024-253-8	Sequence 8, Appl
897	5	1.8	93	4	US-09-107-532A-5880	Sequence 5880, Ap	970	5	1.8	109	2	US-08-646-981-6	Sequence 6, Appl
898	5	1.8	94	1	US-08-262-037-57	Sequence 57, Appl	971	5	1.8	109	3	US-08-982-493-2	Sequence 2, Appl
899	5	1.8	94	3	US-08-232-878-4	Sequence 4, Appl	972	5	1.8	109	3	US-09-188-930-329	Sequence 329, App
900	5	1.8	96	1	US-08-538-878B-35	Sequence 35, Appl	973	5	1.8	109	4	US-09-199-637A-89	Sequence 89, Appl
901	5	1.8	96	1	US-08-442-063A-33	Sequence 33, Appl	974	5	1.8	109	4	US-09-399-913-34	Sequence 34, Appl
902	5	1.8	96	1	US-08-294-522B-34	Sequence 34, Appl	975	5	1.8	109	4	US-09-298-731-34	Sequence 34, Appl
903	5	1.8	96	2	US-08-807-861A-35	Sequence 35, Appl	976	5	1.8	109	4	US-09-312-283C-329	Sequence 329, App

Sequence 422, App  
Sequence 334, App  
Sequence 40, Appl  
Sequence 121, App  
Sequence 40, Appl  
Sequence 53, Appl  
Sequence 115, App  
Sequence 244, App  
Sequence 37, Appl  
Sequence 43, Appl  
Sequence 43, Appl  
Sequence 37, Appl  
Sequence 6, Appl  
Sequence 4, Appl  
Sequence 822, App  
Sequence 244, App  
Sequence 2, Appl  
Sequence 81, Appl  
Sequence 4, Appl  
Sequence 4, Appl  
Sequence 304, App  
Sequence 26817, A  
Sequence 6182, App  
Sequence 58, Appl

ALIGNMENTS

RESULT 1  
US-09-385-028-11  
; Sequence 11, Application US/09385028  
; Patent No. 6232106  
; GENERAL INFORMATION:  
; APPLICANT: Susan E. Jensen  
; APPLICANT: Kwamena A Aidoo  
; APPLICANT: Ashish S. Paradkar  
; TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic  
; Patent No. 6232106  
; TITLE OF INVENTION: Acid Biosynthesis  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PLLC  
; STREET: The Jennifer Building, 400 Seventh Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09385,028  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/790,462  
; FILING DATE: 29-JAN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: D. Douglas Price  
; REGISTRATION NUMBER: 24,514  
; REFERENCE/DOCKET NUMBER: 1418/P57452US2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 638-6666  
; TELEFAX: (202) 39305350  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 248 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single

; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-385-028-11  
Query Match 2.9%; Score 8; DB 3; Length 248;  
Best Local Similarity 100.0%; Pred. No. 6.8; 0; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 13 GKVALITG 20  
Db 7 GKVALITG 14  
RESULT 2  
US-09-726-614-11  
; Sequence 11, Application US/09726614  
; Patent No. 6514735  
; GENERAL INFORMATION:  
; APPLICANT: Susan E. Jensen  
; APPLICANT: Kwamena A Aidoo  
; APPLICANT: Ashish S. Paradkar  
; TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic  
; Patent No. 6514735  
; TITLE OF INVENTION: Acid Biosynthesis  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PLLC  
; STREET: The Jennifer Building, 400 Seventh Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09726,614  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/790,462  
; FILING DATE: 29-JAN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: D. Douglas Price  
; REGISTRATION NUMBER: 24,514  
; REFERENCE/DOCKET NUMBER: 1418/P57452US2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 638-6666  
; TELEFAX: (202) 39305350  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 248 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-726-614-11  
Query Match 2.9%; Score 8; DB 4; Length 248;  
Best Local Similarity 100.0%; Pred. No. 6.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 13 GKVALITG 20  
Db 7 GKVALITG 14  
RESULT 3  
US-09-328-352-5742  
; Sequence 5742, Application US/09328352

; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03FA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 5742  
; LENGTH: 262  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-5742

Query Match 2.9%; Score 8; DB 4; Length 262;  
Best Local Similarity 100.0%; Pred. No. 7.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 KQUALITG 20  
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Db 18 GKVALITG 25

RESULT 4  
US-09-252-991A-19626  
; Sequence 19626, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 19626  
; LENGTH: 267  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-19626

Query Match 2.9%; Score 8; DB 4; Length 267;  
Best Local Similarity 100.0%; Pred. No. 7.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 185 IRVNCCLSP 192  
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Db 196 IRVNCCLSP 203

RESULT 5  
US-09-134-001C-4339  
; Sequence 4339, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 4339  
; LENGTH: 290

; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-4339

Query Match 2.9%; Score 8; DB 4; Length 290;  
Best Local Similarity 100.0%; Pred. No. 7.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 KQUALITGG 21  
| | | | | | | |  
Db 46 KQUALITGG 53

RESULT 6  
US-09-026-482B-2  
; Sequence 2, Application US/09026482B  
; Patent No. 6143538  
; GENERAL INFORMATION:  
; APPLICANT: REISER, STEVEN E.  
; APPLICANT: SOMMERVILLE, CHRIS  
; TITLE OF INVENTION: ACYL-COA REDUCTASE  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PAUL A. GOTTLIEB, AGCTT  
; ADDRESSEE: DEPARTMENT OF ENERGY  
; ADDRESSEE: GC-62 (FORSTL) MS-6F-067  
; STREET: 1000 INDEPENDENCE AVE. S.W.  
; CITY: WASHINGTON, D.C.  
; ZIP: 20585  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORDPERFECT 6.22  
; CURRENT APPLICATION DATA: US/09/026,482B  
; APPLICATION NUMBER: 02/19/98  
; FILING DATE: 02/19/98  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ALWAN, JOY  
; REGISTRATION NUMBER: 40486  
; REFERENCE/DOCKET NUMBER: S-87814  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 630-252-2179  
; TELEFAX: 630-252-2779  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 295 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-026-482B-2

Query Match 2.9%; Score 8; DB 3; Length 295;  
Best Local Similarity 100.0%; Pred. No. 8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 KQUALITG 20  
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Db 15 GKVALITG 22

RESULT 7  
US-08-580-545B-2  
; Sequence 2, Application US/08580545B  
; Patent No. 5932713  
; GENERAL INFORMATION:  
; APPLICANT: Yoshihisa, Kasukabe  
; APPLICANT: Koichi, Fujisawa  
; APPLICANT: Susumu, Nishiguchi  
; APPLICANT: Yoshihiko, Maekawa  
; APPLICANT: Randy, Allen  
; TITLE OF INVENTION: COTTON FIBER TISSUE-SPECIFIC GENES

```
;
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 601 Thirteenth Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,545B
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bretschneider, Barry E.
; REGISTRATION NUMBER: 28,055
; REFERENCE/DOCKET NUMBER: 04473/068001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/783-2331
; TELEFAX: 202/783-5070
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 323 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-580-545B-2

Query Match 2.9%; Score 8; DB 2; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 19 TGGASGIG 26
Db 40 TGGASGIG 47

;
; RESULT 8
; US-09-262-653A-2
; Sequence 2, Application US/09262653A
; Patent No. 6168294
; GENERAL INFORMATION:
; APPLICANT: Yoshihisa, Kasukabe
; APPLICANT: Koichi, Fujisawa
; APPLICANT: Susumu, Nishiguchi
; APPLICANT: Yoshihiko, Maekawa
; APPLICANT: Randy, Allen
; TITLE OF INVENTION: COTTON FIBER TISSUE-SPECIFIC GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 601 Thirteenth Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/262,653A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bretschneider, Barry E.
; REGISTRATION NUMBER: 28,055
; REFERENCE/DOCKET NUMBER: 04473/068001
;

;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/783-5070
; TELEFAX: 202/783-2331
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 323 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-262-653A-2

Query Match 2.9%; Score 8; DB 3; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 19 TGGASGIG 26
Db 40 TGGASGIG 47

;
; RESULT 9
; US-09-328-352-4279
; Sequence 4279, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4279
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
; US-09-328-352-4279

Query Match 2.6%; Score 7; DB 4; Length 87;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 140 RSGNIIS 146
Db 65 RSGNIIS 71

;
; RESULT 10
; US-09-252-991A-21618
; Sequence 21618, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21618
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-21618

Query Match 2.6%; Score 7; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 176 LAVELGQ 182  
Db 47 LAVELGQ 53

RESULT 11  
US-09-252-991A-18834  
; Sequence 18834, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252.991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 18834  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-18834

Query Match 2.6%; Score 7; DB 4; Length 175;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 133 ARVMIPA 139  
Db 108 ARVMIPA 114

RESULT 12  
US-09-648-004-20  
; Sequence 20, Application US/09648004  
; Patent No. 6498242  
; GENERAL INFORMATION:  
; APPLICANT: CHEN, QIONG  
; APPLICANT: THOMAS, STUART  
; APPLICANT: NAGARAJAN, VASANTHA  
; TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND  
; TITLE OF INVENTION: INTERMEDIATES  
; FILE REFERENCE: CL-1341-A  
; CURRENT APPLICATION NUMBER: US/09/648.004  
; CURRENT FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/252.553  
; PRIOR FILING DATE: 1999-02-19  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Microsoft Office 97  
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; Sequence 2, Application US/08815225  
; Patent No. 6268479  
; GENERAL INFORMATION:  
; APPLICANT: Stern, David M.  
; APPLICANT: Yan, Shi Du  
; TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE  
; TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/815,225  
; FILING DATE: 12-MAR-1997  
; CLASSIFICATION: 536

; APPLICANT: Stern, David M.  
; APPLICANT: Yan, Shi Du  
; TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE  
; TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
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; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/815,225  
; FILING DATE: 12-MAR-1997  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/55209  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
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; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-815-225-2

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; GENERAL INFORMATION:  
; APPLICANT: Stern, David M.  
; APPLICANT: Yan, Shi Du  
; TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE  
; TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: U.S.A.  
; ZIP: 10036  
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; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/815,225  
; FILING DATE: 12-MAR-1997  
; CLASSIFICATION: 536

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; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/55209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 3:
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; FILE REFERENCE: 25885-1651
; CURRENT APPLICATION NUMBER: US/09/347,878C
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6	7	2.6	53	10	Sequence 473, App
7	7	2.6	53	11	Sequence 128, App
8	7	2.6	53	11	Sequence 128, App
9	7	2.6	53	15	Sequence 128, App
10	7	2.6	92	15	Sequence 128, App
11	7	2.6	181	12	Sequence 4341, Ap
12	7	2.6	199	9	Sequence 45, Appl
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149	6	2, 2	148	12	US-10-173-702-360	Sequence 360, App	222	6	2, 2	148	15	US-10-176-493-360	Sequence 360, App
150	6	2, 2	148	12	US-10-173-703-360	Sequence 360, App	223	6	2, 2	148	15	US-10-176-756-360	Sequence 360, App
151	6	2, 2	148	12	US-10-173-704-360	Sequence 360, App	224	6	2, 2	148	15	US-10-176-911-360	Sequence 360, App
152	6	2, 2	148	12	US-10-174-574-360	Sequence 360, App	225	6	2, 2	148	15	US-10-176-919-360	Sequence 360, App
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236	6	2.2	148	15	US-10-180-559-360	Sequence 360, App	309	6	2.2	148	15	US-10-179-507-360	Sequence 360, App
237	6	2.2	148	15	US-10-181-000-360	Sequence 360, App	310	6	2.2	148	15	US-10-179-516-360	Sequence 360, App
238	6	2.2	148	15	US-10-183-010-360	Sequence 360, App	311	6	2.2	148	15	US-10-179-519-360	Sequence 360, App
239	6	2.2	148	15	US-10-183-012-360	Sequence 360, App	312	6	2.2	148	15	US-10-179-525-360	Sequence 360, App
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259	6	2.2	148	15	US-10-180-543-360	Sequence 360, App	332	6	2.2	148	15	US-10-197-695-360	Sequence 360, App
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397	6	2.2	148	15	US-10-195-890-360	Sequence 360, App	470	6	2.2	148	15	US-10-197-703-360	Sequence 360, App
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431	6	2.2	148	15	US-10-196-758-360	Sequence 360, App	504	6	2.2	148	15	US-10-205-894-360	Sequence 360, App
432	6	2.2	148	15	US-10-198-770-360	Sequence 360, App	505	6	2.2	148	15	US-10-205-896-360	Sequence 360, App
433	6	2.2	148	15	US-10-199-308-360	Sequence 360, App	506	6	2.2	148	15	US-10-205-898-360	Sequence 360, App
434	6	2.2	148	15	US-10-206-617-360	Sequence 360, App	507	6	2.2	148	15	US-10-205-901-360	Sequence 360, App
435	6	2.2	148	15	US-10-208-893-360	Sequence 360, App	508	6	2.2	148	15	US-10-206-903-360	Sequence 360, App
436	6	2.2	148	15	US-10-208-897-360	Sequence 360, App	509	6	2.2	148	15	US-10-206-909-360	Sequence 360, App
437	6	2.2	148	15	US-10-208-897-360	Sequence 360, App	510	6	2.2	148	15	US-10-206-911-360	Sequence 360, App
438	6	2.2	148	15	US-10-196-754-360	Sequence 360, App	511	6	2.2	148	15	US-10-206-911-360	Sequence 360, App
439	6	2.2	148	15	US-10-174-571-360	Sequence 360, App	512	6	2.2	148	15	US-10-206-911-360	Sequence 360, App
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443	6	2.2	148	15	US-10-184-633-360	Sequence 360, App	516	6	2.2	148	15	US-10-206-921-360	Sequence 360, App
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532	6	2.2	148	15	US-10-208-030-360	Sequence 360, App	605	6	2.2	148	15	US-10-223-090-242	Sequence 242, App
533	6	2.2	148	15	US-10-015-933A-336	Sequence 336, App	606	6	2.2	148	15	US-10-223-087-242	Sequence 242, App
534	6	2.2	148	15	US-10-232-232-360	Sequence 360, App	607	6	2.2	148	15	US-10-011-692A-336	Sequence 336, App
535	6	2.2	148	15	US-10-195-898-360	Sequence 360, App	608	6	2.2	148	15	US-10-006-768A-336	Sequence 336, App
536	6	2.2	148	15	US-10-196-759-360	Sequence 360, App	609	6	2.2	148	15	US-10-017-610A-336	Sequence 336, App
537	6	2.2	148	15	US-10-015-869A-336	Sequence 336, App	610	6	2.2	148	15	US-10-198-760-360	Sequence 360, App
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547	6	2.2	148	15	US-10-195-895-360	Sequence 360, App	620	6	2.2	148	15	US-10-187-755-360	Sequence 360, App
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554	6	2.2	148	15	US-10-207-924-360	Sequence 360, App	627	6	2.2	151	9	US-10-091-438-199	Sequence 199, App
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563	6	2.2	148	15	US-10-006-117A-336	Sequence 336, App	636	6	2.2	158	11	US-09-892-877-291	Sequence 291, App
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572	6	2.2	148	15	US-10-187-592-360	Sequence 360, App	645	6	2.2	176	12	US-09-882-171-440	Sequence 440, App
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575	6	2.2	148	15	US-10-198-771-360	Sequence 360, App	648	6	2.2	191	15	US-10-106-698-6213	Sequence 6213, App
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579	6	2.2	148	15	US-10-201-325-360	Sequence 360, App	652	6	2.2	220	10	US-09-738-626-4189	Sequence 4189, App
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588	6	2.2	148	15	US-10-179-511-360	Sequence 360, App	661	6	2.2	239	16	US-10-278-536-204	Sequence 204, App
589	6	2.2	148	15	US-10-179-518-360	Sequence 360, App	662	6	2.2	241	15	US-10-102-806-610	Sequence 610, App
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597	6	2.2	148	15	US-10-202-938-360	Sequence 360, App	670	6	2.2	245	9	US-09-796-089-9	Sequence 9, Appl1
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691	6	2.2	245	15	US-10-238-183-82	Sequence 82, Appl	764	245	15	US-10-245-852-82	Sequence 82, Appl
692	6	2.2	245	15	US-10-238-370-82	Sequence 82, Appl	765	245	15	US-10-245-881-82	Sequence 82, Appl
693	6	2.2	245	15	US-10-238-370-82	Sequence 82, Appl	766	245	15	US-10-245-911-82	Sequence 82, Appl
694	6	2.2	245	15	US-10-245-055-82	Sequence 82, Appl	767	245	15	US-10-245-913-82	Sequence 82, Appl
695	6	2.2	245	15	US-10-245-147-82	Sequence 82, Appl	768	245	15	US-10-246-080-82	Sequence 82, Appl
696	6	2.2	245	15	US-10-245-730-82	Sequence 82, Appl	769	245	15	US-10-246-121-82	Sequence 82, Appl
697	6	2.2	245	15	US-10-245-739-82	Sequence 82, Appl	770	245	15	US-10-246-305-82	Sequence 82, Appl
698	6	2.2	245	15	US-10-246-210-82	Sequence 82, Appl	771	245	15	US-10-247-036-82	Sequence 82, Appl
699	6	2.2	245	15	US-10-239-196-82	Sequence 82, Appl	772	245	15	US-10-168-274-25	Sequence 25, Appl
700	6	2.2	245	15	US-10-243-024-82	Sequence 82, Appl	773	245	15	US-10-243-255-82	Sequence 82, Appl
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711	6	2.2	245	15	US-10-246-976-82	Sequence 82, Appl	784	253	11	US-09-864-455-184	Sequence 184, App
712	6	2.2	245	15	US-10-243-320-82	Sequence 82, Appl	785	257	9	US-09-864-761-37608	Sequence 37608, A
713	6	2.2	245	15	US-10-242-743-82	Sequence 82, Appl	786	257	9	US-09-815-242-11706	Sequence 11706, A
714	6	2.2	245	15	US-10-242-845-82	Sequence 82, Appl	787	257	15	US-10-156-761-12528	Sequence 12528, A
715	6	2.2	245	15	US-10-237-636-82	Sequence 82, Appl	788	258	15	US-10-156-055A-1	Sequence 1, Appl
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718	6	2.2	245	15	US-10-238-411-82	Sequence 82, Appl	791	266	14	US-10-067-989-3	Sequence 3, Appl
719	6	2.2	245	15	US-10-243-124-82	Sequence 82, Appl	792	267	9	US-09-735-643-63	Sequence 63, Appl
720	6	2.2	245	15	US-10-243-425-82	Sequence 82, Appl	793	267	14	US-10-042-141-63	Sequence 63, Appl
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722	6	2.2	245	15	US-10-245-874-82	Sequence 82, Appl	795	273	12	US-10-289-795-13	Sequence 13, Appl
723	6	2.2	245	15	US-10-242-653-82	Sequence 82, Appl	796	274	10	US-09-976-059-17	Sequence 17, Appl
724	6	2.2	245	15	US-10-243-167-82	Sequence 82, Appl	797	278	12	US-09-866-034-2	Sequence 2, Appl
725	6	2.2	245	15	US-10-243-388-82	Sequence 82, Appl	798	278	12	US-10-210-951-60	Sequence 60, Appl
726	6	2.2	245	15	US-10-244-947-82	Sequence 82, Appl	799	278	12	US-10-211-884-60	Sequence 60, Appl
727	6	2.2	245	15	US-10-244-968-82	Sequence 82, Appl	800	278	13	US-10-033-246-2	Sequence 2, Appl
728	6	2.2	245	15	US-10-244-990-82	Sequence 82, Appl	801	278	13	US-10-033-301-2	Sequence 2, Appl
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740	6	2.2	245	15	US-10-247-058-82	Sequence 82, Appl	813	282	12	US-09-815-242-5592	Sequence 5592, Ap
741	6	2.2	245	15	US-10-245-454-82	Sequence 82, Appl	814	286	11	US-09-910-600-14	Sequence 14, Appl
742	6	2.2	245	15	US-10-237-471-82	Sequence 82, Appl	815	286	15	US-10-106-698-5072	Sequence 5072, Ap
743	6	2.2	245	15	US-10-238-261-82	Sequence 82, Appl	816	287	15	US-09-216-393-341	Sequence 341, App
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821	6	2.2	290	12	US-10-238-075-498	Sequence 498, App	894	6	2.2	336	12	US-10-187-749-182	Sequence 182, App
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824	6	2.2	293	9	US-09-815-242-12199	Sequence 12199, A	897	6	2.2	336	12	US-10-184-642-182	Sequence 182, App
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830	6	2.2	296	10	US-09-718-626-6533	Sequence 6533, Ap	903	6	2.2	336	12	US-10-173-694-182	Sequence 182, App
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832	6	2.2	299	12	US-10-295-681-49	Sequence 49, Appl	905	6	2.2	336	12	US-10-173-699-182	Sequence 182, App
833	6	2.2	300	15	US-10-156-761-7996	Sequence 7996, Ap	906	6	2.2	336	12	US-10-173-707-182	Sequence 182, App
834	6	2.2	301	15	US-10-156-761-14802	Sequence 14802, A	907	6	2.2	336	12	US-10-174-569-182	Sequence 182, App
835	6	2.2	309	15	US-10-156-761-11336	Sequence 11336, A	908	6	2.2	336	12	US-10-174-583-182	Sequence 182, App
836	6	2.2	310	9	US-09-815-242-10707	Sequence 10707, A	909	6	2.2	336	12	US-10-174-587-182	Sequence 182, App
837	6	2.2	311	12	US-10-032-201B-210	Sequence 210, App	910	6	2.2	336	12	US-10-174-589-182	Sequence 182, App
838	6	2.2	311	12	US-10-032-201B-211	Sequence 211, App	911	6	2.2	336	12	US-10-174-591-182	Sequence 182, App
839	6	2.2	312	10	US-09-761-640-8	Sequence 8, Appli	912	6	2.2	336	12	US-10-175-736-182	Sequence 182, App
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859	6	2.2	326	15	US-10-156-761-12620	Sequence 12620, A	932	6	2.2	336	12	US-10-173-702-182	Sequence 182, App
860	6	2.2	327	9	US-09-925-301-862	Sequence 862, App	933	6	2.2	336	12	US-10-173-703-182	Sequence 182, App
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863	6	2.2	332	12	US-10-278-946-20	Sequence 20, Appl	936	6	2.2	336	12	US-10-176-486-182	Sequence 182, App
864	6	2.2	334	15	US-10-156-761-8246	Sequence 8246, Ap	937	6	2.2	336	12	US-10-176-490-182	Sequence 182, App
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872	6	2.2	336	11	US-09-978-585A-303	Sequence 303, App	945	6	2.2	336	12	US-10-143-029A-303	Sequence 303, App
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ALIGNMENTS

RESULT 1  
 US-09-944-160-24  
 ; Sequence 24, Application US/09944160  
 ; Patent No. US20020174452A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lewis, No. US20020174452A1man  
 ; APPLICANT: Davin, Laurence  
 ; APPLICANT: .. Huang, Ning  
 ; TITLE OF INVENTION: Monocot Seeds with Increased Lignan  
 ; FILE REFERENCE: WSUR117983  
 ; CURRENT APPLICATION NUMBER: US/09/944,160  
 ; PRIOR FILING DATE: 2001-08-30  
 ; PRIOR FILING DATE: 2000-09-07  
 ; NUMBER OF SEQ ID NOS: 49  
 ; SOFTWARE: Fast-Seq for Windows Version 4.0  
 ; SEQ ID NO 24  
 ; LENGTH: 276  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: secisolaricresinol dehydrogenase amino acid  
 ; OTHER INFORMATION: sequence from plasmid pAPI249  
 US-09-944-160-24

Query Match 12.5%; Score 34; DB 10; Length 276;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-25;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 63 SNSTYIHCDVTNEDGVKNAVDNTVSTYKGLDIMP 96  
 RESULT 2  
 US-10-156-761-14812  
 ; Sequence 14812, Application US/10156761  
 ; Publication No. US20030119018A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: OMURA, SATOSHI  
 ; APPLICANT: IKEDA, HARUO  
 ; APPLICANT: ISHIKAWA, JUN  
 ; APPLICANT: HORIKAWA, HIROSHI  
 ; APPLICANT: SHIBA, TADAYOSHI  
 ; APPLICANT: SAKAKI, YOSHIYUKI  
 ; APPLICANT: HATTORI, MASAHIRA  
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
 ; FILE REFERENCE: 249-262  
 ; CURRENT APPLICATION NUMBER: US/10/156,761  
 ; PRIOR FILING DATE: 2002-05-29  
 ; PRIOR FILING DATE: 2001-05-30  
 ; PRIOR FILING DATE: 2001-05-30  
 ; PRIOR FILING DATE: 2001-08-02  
 ; NUMBER OF SEQ ID NOS: 15109  
 ; SEQ ID NO 14812  
 ; LENGTH: 251  
 ; TYPE: PRT  
 ; ORGANISM: Streptomyces avermitilis  
 US-10-156-761-14812

Query Match 2.9%; Score 8; DB 15; Length 251;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TGGASGIG 26  
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 Db 12 TGGASGIG 19

RESULT 3  
 US-10-156-761-14537-  
 ; Sequence 14537, Application US/10156761  
 ; Publication No. US20030119018A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: OMURA, SATOSHI  
 ; APPLICANT: IKEDA, HARUO  
 ; APPLICANT: ISHIKAWA, JUN  
 ; APPLICANT: HORIKAWA, HIROSHI  
 ; APPLICANT: SHIBA, TADAYOSHI  
 ; APPLICANT: SAKAKI, YOSHIYUKI  
 ; APPLICANT: HATTORI, MASAHIRA  
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
 ; FILE REFERENCE: 249-262  
 ; CURRENT APPLICATION NUMBER: US/10/156,761  
 ; PRIOR FILING DATE: 2002-05-29  
 ; PRIOR FILING DATE: 2001-05-30  
 ; PRIOR FILING DATE: 2001-05-30  
 ; PRIOR FILING DATE: 2001-08-02  
 ; NUMBER OF SEQ ID NOS: 15109  
 ; SEQ ID NO 14537  
 ; LENGTH: 253  
 ; TYPE: PRT  
 ; ORGANISM: Streptomyces avermitilis  
 US-10-156-761-14537

Query Match 2.9%; Score 8; DB 15; Length 253;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GKVALITG 20  
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 Db 9 GKVALITG 16

Best Local Similarity 100.0%; Pred. No. 17;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TGGASGIG 26  
Db 15 TGGASGIG 22

## RESULT 6

US-09-984-245-128  
; Sequence 128, Application US/09984245  
; Patent No. US20020165374A1  
; GENERAL INFORMATION:  
; APPLICANT: Young et al.  
; TITLE OF INVENTION: 87 Human Secreted Proteins  
; FILE REFERENCE: P2004P1  
; CURRENT APPLICATION NUMBER: US/09/984,245  
; CURRENT FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: 09/154,707  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: PCT/US98/05311  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: US 60/041,277  
; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: US 60/042,344  
; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: US 60/041,276  
; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: US 60/041,281  
; PRIOR FILING DATE: 1997-03-21  
; PRIOR APPLICATION NUMBER: US 60/048,094  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,350  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,188  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,135  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/050,937  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,187  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,099  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,352  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,186  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,069  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,095  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,131  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,096  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,351  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/048,154  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: US 60/054,804  
; PRIOR FILING DATE: 1997-08-05  
; PRIOR APPLICATION NUMBER: US 60/056,370  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: US 60/060,862  
; PRIOR FILING DATE: 1997-10-02  
; NUMBER OF SEQ ID NOS: 343  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 128

## RESULT 4

US-09-815-242-10597  
; Sequence 10597, Application US/09815242  
; Patent No. US2002061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10597  
; LENGTH: 262  
; TYPE: PRT  
; ORGANISM: Enterococcus faecalis

Query Match 2.9%; Score 8; DB 9; Length 262;

Best Local Similarity 100.0%; Pred. No. 17;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GKVALITG 20  
Db 12 GKVALITG 19

## RESULT 5

US-10-238-075-473  
; Sequence 473, Application US/10238075  
; Publication No. US2003014832A1  
; GENERAL INFORMATION:  
; APPLICANT: I. N. S. E. R. M.  
; TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolated  
; FILE REFERENCE: BLANDINE  
; CURRENT APPLICATION NUMBER: US/10/238,075  
; CURRENT FILING DATE: 2002-09-10  
; PRIOR APPLICATION NUMBER: 0003145  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 1576  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 473  
; LENGTH: 268  
; TYPE: PRT  
; ORGANISM: Escherichia coli  
US-10-238-075-473

Query Match 2.9%; Score 8; DB 12; Length 268;

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; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-245-128

Query Match          2.6%; Score 7; DB 10; Length 53;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ITGGASG 24
Db 15 ITGGASG 21

RESULT 7
US-09-966-262-128
; Sequence 128, Application US/09966262
; Publication No. US20030050461A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US 09/966,262
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: US 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
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; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 128
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-966-262-128

Query Match          2.6%; Score 7; DB 11; Length 53;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ITGGASG 24
Db 15 ITGGASG 21

RESULT 8
US-09-983-966-128
; Sequence 128, Application US/09983966
; Publication No. US20030060619A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US 09/983,966
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
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; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
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; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 128
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-983-966-128

Query Match      2.6%; Score 7; DB 11; Length 53;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ITGGASG 24
Db 15 ITGGASG 21

RESULT 9
US-10-143-090-128
; Sequence 128, Application US/10143090
; Publication No. US20030069406A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; CURRENT APPLICATION NUMBER: US/10/143,090
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 128
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-143-090-128

Query Match      2.6%; Score 7; DB 15; Length 53;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ITGGASG 24
Db 15 ITGGASG 21

RESULT 10
US-10-106-698-4341
; Sequence 4341, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
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; SEQ ID NO 4341
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MISC_FEATURE
; LOCATION: (49)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-4341

Query Match      2.6%; Score 7; DB 15; Length 92;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 GIGETTA 30
Db 80 GIGETTA 86

RESULT 11
US-10-291-190-45
; Sequence 45, Application US/10291190
; Publication No. US20030171549A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Park, Rfances
; APPLICANT: Gajiwala, Ketan S.
; APPLICANT: Buchanan, Sean Grant
; APPLICANT: Sauder, J. Michael
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF YIIM PROTEINS
; FILE REFERENCE: 52498-20009.00
; CURRENT APPLICATION NUMBER: US/10/291,190
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 60/337,769
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 181
; TYPE: PRT
; ORGANISM: D. radiodurans (15806071)
US-10-291-190-45

Query Match      2.6%; Score 7; DB 12; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 RVLNVV 122
Db 2 RVLNVV 8

RESULT 12
US-09-815-242-13753
; Sequence 13753, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Hasebeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITEA 011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
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; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13753
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Salmonella typhi
US-09-815-242-13753

Query Match      2.6%; Score 7; DB 9; Length 199;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      196 PTALGKK 202
DB      98 PTALGKK 104

RESULT 13
US-09-811-284-144
; Sequence 144, Application US/09811284
; Patent No. US20020058306A1
; GENERAL INFORMATION:
; APPLICANT: vogelli, Gabriel
; TITLE OF INVENTION: No. US20020058306A1el G Protein-Coupled Receptors
; FILE REFERENCE: 00167U81
; CURRENT APPLICATION NUMBER: US/09/811,284
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/189,783
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/189,907
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/189,918
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/189,960
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/189,917
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/192,945
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/192,916
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/192,923
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/192,933
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/192,830
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/192,234
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/192,155
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,935
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 258
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 144
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-811-284-144

Query Match      2.6%; Score 7; DB 9; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Best Local Similarity 100.0%; Pred. No. 1.3e+02;
; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      146 STASLSS 152
DB      131 STASLSS 137

RESULT 14
US-10-156-761-9390
; Sequence 9390, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9390
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9390

Query Match      2.6%; Score 7; DB 15; Length 233;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 VALITGG 21
DB      6 VALITGG 12

RESULT 15
US-10-272-419-20
; Sequence 20, Application US/10272419
; Publication No. US20030087403A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, QIONG
; APPLICANT: THOMAS, STUART
; APPLICANT: NAGARAJAN, VASANTHA
; TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND
; FILE REFERENCE: C11341.1A
; CURRENT APPLICATION NUMBER: US/10/272,419
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 09/252,553
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 20
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Acinetobacter sp.
US-10-272-419-20

Query Match      2.6%; Score 7; DB 15; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 KVALITG 20
DB      6 KVALITG 12

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Db 12 KVALITG 18

Search completed: October 23, 2003, 13:15:07  
Job time : 110 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 23, 2003, 12:59:30 ; Search time 40 Seconds  
(without alignments)

656.351 Million cell updates/sec

Title: US-09-673-918a-2

Perfect score: 273

Sequence: 1 MQLRTAFARLEKGVALTG.....IDGGFVCNEVIKVFQYPS 273

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

PIR\_76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	6-2	234	2 T03734	short chain alcohol
2	17	6-2	284	2 T02257	probable alcohol d
3	16	5-9	283	2 H85039	probable short cha
4	13	4-8	267	2 T11579	probable short cha
5	10	3-7	255	1 S39737	glucose 1-dehydrog
6	10	3-7	255	2 C87434	2-deoxy-D-gluconat
7	10	3-7	256	2 AD2307	hypothetical prote
8	10	3-7	262	2 AB3545	toluenesulfonate z
9	10	3-7	285	2 F96563	hypothetical prote
10	9	3-3	15	2 PC4213	bphB protein - Com
11	9	3-3	245	2 B82680	pteridine reductas
12	9	3-3	257	2 T02175	probable alcohol d
13	9	3-3	258	2 T02176	probable alcohol d
14	9	3-3	258	2 H75616	probable alcohol d
15	9	3-3	259	2 A13149	oxidoreductase, sh
16	9	3-3	259	2 H98137	3-oxoacyl-(acyl-ca
17	9	3-3	264	2 T02174	probable alcohol d
18	9	3-3	272	2 AC3359	glucose 1-dehydrog
19	9	3-3	275	2 C70814	hypothetical prote
20	9	3-3	286	2 D69768	alcohol dehydrogen
21	9	3-3	287	2 G83838	oxidoreductase (sh
22	9	3-3	288	2 C96590	hypothetical prote
23	9	3-3	303	2 T74604	short-chain alcohol
24	9	3-3	689	2 H70024	sorbitol-6-phospha
25	8	2-9	158	2 AD3301	2-deoxy-D-gluconat
26	8	2-9	240	2 H75014	3-oxoacyl-(acyl-ca
27	8	2-9	248	2 B97223	probable 3-ketoacy
28	8	2-9	252	2 B90495	hypothetical prote
29	8	2-9	253	1 S17711	probable dehydroge

30	8	2-9	254	2 E85069	hypothetical prote
31	8	2-9	256	2 B95274	probable oxidoredu
32	8	2-9	260	2 A84695	probable tropinone
33	8	2-9	262	2 B84695	probable tropinone
34	8	2-9	262	2 C84711	probable tropinone
35	8	2-9	285	2 D84643	probable ATP-depen
36	8	2-9	267	2 S50186	sorbitol-6-phospha
37	8	2-9	268	2 C91254	probable sorbitol-
38	8	2-9	268	2 G86094	D-glucitol-6-phosp
39	8	2-9	277	1 F42409	cis-2,3-dihydrobip
40	8	2-9	277	1 JN0814	cis-2,3-dihydrobip
41	8	2-9	277	2 JW0102	azarene carbazole
42	8	2-9	278	2 C75616	oxidoreductase, sh
43	8	2-9	279	2 T21410	hypothetical prote
44	8	2-9	285	2 AF2453	oxidoreductase alr
45	8	2-9	296	2 B87260	hypothetical prote
46	8	2-9	299	2 D97075	probable dehydroge
47	8	2-9	449	2 I40178	probable glutathio
48	8	2-9	629	2 D96533	ARP protein limpor
49	8	2-9	629	2 S57614	ARP protein - Arab
50	8	2-9	657	2 S77543	short-chain alcoho
51	7	2-6	111	2 H72707	hypothetical prote
52	7	2-6	133	2 T43374	ribosomal protein
53	7	2-6	136	2 T40638	60s ribosomal prot
54	7	2-6	141	2 G72661	hypothetical prote
55	7	2-6	146	2 A71115	hypothetical prote
56	7	2-6	153	2 A55139	myoglobin, body wa
57	7	2-6	154	2 T19332	hypothetical prote
58	7	2-6	159	2 B83245	hypothetical prote
59	7	2-6	167	1 F1SP5	photosystem I chai
60	7	2-6	172	2 B75338	thermoresistant gl
61	7	2-6	181	2 D75443	conserved hypothet
62	7	2-6	188	2 AB0744	probable hydrolase
63	7	2-6	191	1 G69292	tryptophan repress
64	7	2-6	200	2 T02173	probable alcohol d
65	7	2-6	207	2 T32882	hypothetical prote
66	7	2-6	214	2 G70348	conserved hypothet
67	7	2-6	215	2 T39928	probable transcrip
68	7	2-6	217	2 B83643	conserved hypothet
69	7	2-6	231	2 S37778	filamin, muscle -
70	7	2-6	232	2 B82531	50S ribosomal prot
71	7	2-6	233	2 B90088	similar to proteas
72	7	2-6	243	2 AF3105	oxidoreductase Atu
73	7	2-6	245	2 AG3436	short-chain dehydr
74	7	2-6	246	2 AH0190	probable oxidoredu
75	7	2-6	248	2 F82128	3-oxoacyl-(acyl-ca
76	7	2-6	248	2 AF0177	probable beta-keto
77	7	2-6	248	2 AG3007	short-chain dehydr
78	7	2-6	248	2 G98276	short-chain dehydr
79	7	2-6	251	2 T06364	probable short-cha
80	7	2-6	252	2 E72612	hypothetical prote
81	7	2-6	255	2 T15987	hypothetical prote
82	7	2-6	255	2 D70635	hypothetical prote
83	7	2-6	255	2 S54515	probable membrane
84	7	2-6	257	2 AD2934	short chain dehydr
85	7	2-6	257	2 C98348	reductase (Al13282
86	7	2-6	261	2 B87279	hypothetical prote
87	7	2-6	261	2 E82748	tropinone reductas
88	7	2-6	261	2 AF2945	dehydrogenase Atu3
89	7	2-6	261	2 AG2810	short chain dehydr
90	7	2-6	261	2 B97589	1-2,3-butanediol d
91	7	2-6	261	2 D98337	L-iditol sorbitol d
92	7	2-6	264	2 F98181	oxidoreductase ucp
93	7	2-6	271	2 AE3150	dehydrogenase Atu4
94	7	2-6	271	2 D98137	2,5-dichloro-2,5-c
95	7	2-6	281	2 F69400	2-deoxy-D-gluconat
96	7	2-6	283	2 S41412	tetrahydroxynaphth
97	7	2-6	286	2 G83378	probable short-cha
98	7	2-6	295	2 S50729	sporulation protei
99	7	2-6	297	2 T09396	hypothetical prote
100	7	2-6	305	2 S35991	C-alpha-dehydrogen
101	7	2-6	323	2 AC2481	hypothetical prote
102	7	2-6	328	2 E83504	probable oxidoredu

103	7	2.6	328	2	E70695	probable oxidoreductase	176	6	2.2	87	2	I40094	hypothetical protein
104	7	2.6	339	2	S62596	ubiquinol-cytochrome c reductase	177	6	2.2	87	2	S20740	ubiquinol-cytochrome c reductase
105	7	2.6	359	2	A22212	hypothetical protein	178	6	2.2	88	2	AC2723	ubiquinol-cytochrome c reductase
106	7	2.6	362	2	AG3428	hypothetical protein	179	6	2.2	88	2	S36317	ubiquinol-cytochrome c reductase
107	7	2.6	368	2	T20182	hypothetical protein	180	6	2.2	89	2	S78699	flagellar biosynthesis
108	7	2.6	372	2	G90983	GDP-mannose dehydratase	181	6	2.2	89	2	AE0753	flagellar biosynthesis
109	7	2.6	372	2	B85829	GDP-mannose dehydratase	182	6	2.2	92	2	B90783	flagellar biosynthesis
110	7	2.6	372	2	S28470	GDP-mannose dehydratase	183	6	2.2	92	2	C86685	flagellar biosynthesis
111	7	2.6	373	2	D64971	GDP-mannose dehydratase	184	6	2.2	95	2	T13259	flagellar biosynthesis
112	7	2.6	373	2	B90986	GDP-mannose dehydratase	185	6	2.2	99	2	G75158	flagellar biosynthesis
113	7	2.6	373	2	E85831	GDP-mannose dehydratase	186	6	2.2	99	2	G75158	flagellar biosynthesis
114	7	2.6	373	2	AB0769	GDP-mannose dehydratase	187	6	2.2	103	2	H72672	hypothetical protein
115	7	2.6	378	2	S44777	GDP-mannose dehydratase	188	6	2.2	104	2	S75225	hypothetical protein
116	7	2.6	382	2	T23798	hypothetical protein	189	6	2.2	104	2	E72758	hypothetical protein
117	7	2.6	390	2	D84367	hypothetical protein	190	6	2.2	105	2	C71635	hypothetical protein
118	7	2.6	395	2	T06132	hypothetical protein	191	6	2.2	107	2	G72496	hypothetical protein
119	7	2.6	398	2	JC4254	hypothetical protein	192	6	2.2	110	2	B71524	hypothetical protein
120	7	2.6	399	2	AC2785	hypothetical protein	193	6	2.2	118	2	D75580	hypothetical protein
121	7	2.6	400	2	D97564	hypothetical protein	194	6	2.2	119	2	S04521	hypothetical protein
122	7	2.6	414	2	D69895	hypothetical protein	195	6	2.2	120	2	AD2862	hypothetical protein
123	7	2.6	425	2	H90415	hypothetical protein	196	6	2.2	123	2	PT0387	hypothetical protein
124	7	2.6	431	2	G73305	hypothetical protein	197	6	2.2	123	2	E81120	hypothetical protein
125	7	2.6	431	2	H87587	hypothetical protein	198	6	2.2	125	2	G90363	hypothetical protein
126	7	2.6	444	2	H87587	hypothetical protein	199	6	2.2	126	2	C97846	hypothetical protein
127	7	2.6	451	2	A83509	hypothetical protein	200	6	2.2	126	2	F95078	hypothetical protein
128	7	2.6	458	2	I33477	hypothetical protein	201	6	2.2	126	2	AF0356	hypothetical protein
129	7	2.6	459	2	AH2426	hypothetical protein	202	6	2.2	126	2	E71925	hypothetical protein
130	7	2.6	466	2	H81697	hypothetical protein	203	6	2.2	126	2	B82481	hypothetical protein
131	7	2.6	466	2	E84132	hypothetical protein	204	6	2.2	126	2	D96518	hypothetical protein
132	7	2.6	475	2	T18487	hypothetical protein	205	6	2.2	126	2	F89989	hypothetical protein
133	7	2.6	502	2	AG3641	hypothetical protein	206	6	2.2	127	2	T04411	hypothetical protein
134	7	2.6	515	2	F83891	hypothetical protein	207	6	2.2	127	2	F69070	hypothetical protein
135	7	2.6	569	2	AF0587	hypothetical protein	208	6	2.2	128	2	B45392	hypothetical protein
136	7	2.6	592	2	JC7709	hypothetical protein	209	6	2.2	128	2	B44281	hypothetical protein
137	7	2.6	601	2	D83238	hypothetical protein	210	6	2.2	130	2	G71042	hypothetical protein
138	7	2.6	609	2	T52524	hypothetical protein	211	6	2.2	130	2	B72702	hypothetical protein
139	7	2.6	643	2	T03518	hypothetical protein	212	6	2.2	133	2	A72675	hypothetical protein
140	7	2.6	648	2	A49646	hypothetical protein	213	6	2.2	133	2	F96323	hypothetical protein
141	7	2.6	724	2	AC2832	hypothetical protein	214	6	2.2	134	2	H72476	hypothetical protein
142	7	2.6	724	2	G97609	hypothetical protein	215	6	2.2	134	2	A71136	hypothetical protein
143	7	2.6	737	1	JV0107	hypothetical protein	216	6	2.2	134	2	AF2552	hypothetical protein
144	7	2.6	796	2	H90644	hypothetical protein	217	6	2.2	136	2	S24346	hypothetical protein
145	7	2.6	796	2	H85495	hypothetical protein	218	6	2.2	137	2	C86332	hypothetical protein
146	7	2.6	796	2	H85495	hypothetical protein	219	6	2.2	137	2	C69501	hypothetical protein
147	7	2.6	796	2	AG0523	hypothetical protein	220	6	2.2	137	2	S74888	hypothetical protein
148	7	2.6	797	2	AB3410	hypothetical protein	221	6	2.2	139	2	S22417	hypothetical protein
149	7	2.6	823	2	G90848	hypothetical protein	222	6	2.2	140	1	HABOKA	hypothetical protein
150	7	2.6	823	2	E85706	hypothetical protein	223	6	2.2	141	1	HABA	hypothetical protein
151	7	2.6	858	2	T03544	hypothetical protein	224	6	2.2	141	1	HABA	hypothetical protein
152	7	2.6	872	2	A83428	hypothetical protein	225	6	2.2	141	1	HABA	hypothetical protein
153	7	2.6	908	2	S49538	hypothetical protein	226	6	2.2	141	1	HABOG	hypothetical protein
154	7	2.6	934	1	S42874	hypothetical protein	227	6	2.2	142	2	B25727	hypothetical protein
155	7	2.6	942	2	S53963	hypothetical protein	228	6	2.2	142	2	B49141	hypothetical protein
156	7	2.6	976	2	T23583	hypothetical protein	229	6	2.2	142	2	A58794	hypothetical protein
157	7	2.6	1036	2	B69368	hypothetical protein	230	6	2.2	142	2	T16898	hypothetical protein
158	7	2.6	1107	2	S61667	hypothetical protein	231	6	2.2	142	2	T18166	hypothetical protein
159	7	2.6	1291	2	E82325	hypothetical protein	232	6	2.2	143	2	T38240	hypothetical protein
160	7	2.6	1291	2	AF1116	hypothetical protein	233	6	2.2	143	2	T29740	hypothetical protein
161	7	2.6	1778	2	T37919	hypothetical protein	234	6	2.2	143	2	A46703	hypothetical protein
162	6	2.2	2670	2	S72888	hypothetical protein	235	6	2.2	145	2	T00987	hypothetical protein
163	6	2.2	51	2	T28608	hypothetical protein	236	6	2.2	145	2	D64760	hypothetical protein
164	6	2.2	57	2	H97490	hypothetical protein	237	6	2.2	150	2	A87323	hypothetical protein
165	6	2.2	61	2	G41476	hypothetical protein	238	6	2.2	150	2	H69514	hypothetical protein
166	6	2.2	62	2	B38309	hypothetical protein	239	6	2.2	152	2	G86303	hypothetical protein
167	6	2.2	66	2	H82791	hypothetical protein	240	6	2.2	152	2	AB2011	hypothetical protein
168	6	2.2	72	2	B70517	hypothetical protein	241	6	2.2	158	2	S54083	hypothetical protein
169	6	2.2	74	2	JC4096	hypothetical protein	242	6	2.2	158	2	H83405	hypothetical protein
170	6	2.2	77	2	C97639	hypothetical protein	243	6	2.2	159	2	G84974	hypothetical protein
171	6	2.2	80	1	H8BH3	hypothetical protein	244	6	2.2	159	2	H87539	hypothetical protein
172	6	2.2	81	2	B84149	hypothetical protein	245	6	2.2	160	2	E71197	hypothetical protein
173	6	2.2	81	2	AG3596	hypothetical protein	246	6	2.2	161	2	E48232	hypothetical protein
174	6	2.2	85	2	JC3290	hypothetical protein	247	6	2.2	161	2	AE1322	hypothetical protein
175	6	2.2	85	2	H83492	hypothetical protein	248	6	2.2	161	2	H88103	hypothetical protein

249 6 2.2 162 2 G70005 hypothetical prote  
 250 6 2.2 163 1 PRSAK staphylokinase - p  
 251 6 2.2 163 2 S02330 staphylokinase - p  
 252 6 2.2 163 2 G89983 STAPHYLOKINASE PRE  
 253 6 2.2 164 2 T31280 benzoate 1,2-dioxy  
 254 6 2.2 165 2 C42485 beta protein homol  
 255 6 2.2 166 2 T49489 related to H+-tran  
 256 6 2.2 167 1 S32716 ribosome releasing  
 257 6 2.2 167 2 E83567 probable bacteriop  
 258 6 2.2 167 2 D82448 hypothetical prote  
 259 6 2.2 168 2 C82484 PPS system, IIA co  
 260 6 2.2 168 2 J05192 contractile tube p  
 261 6 2.2 168 2 T44546 hypothetical prote  
 262 6 2.2 168 2 B96437 unknown protein [i  
 263 6 2.2 168 2 C90209 hypothetical prote  
 264 6 2.2 169 2 D82769 phage-related cont  
 265 6 2.2 169 2 AF0039 probable regulator  
 266 6 2.2 170 2 H84752 probable DOF zinc  
 267 6 2.2 172 2 A71263 hypothetical prote  
 268 6 2.2 174 2 T10075 periplasmic protei  
 269 6 2.2 175 1 S74361 diacylglycerol kin  
 270 6 2.2 175 2 T14775 hypothetical prote  
 271 6 2.2 177 2 AH1613 modulates DNA topo  
 272 6 2.2 178 2 T25432 hypothetical prote  
 273 6 2.2 179 2 AE2235 hypothetical prote  
 274 6 2.2 180 2 G64174 hypothetical prote  
 275 6 2.2 180 2 T00116 hypothetical prote  
 276 6 2.2 180 2 S65026 finger protein XFG  
 277 6 2.2 180 2 A83220 ECF family sigma f  
 278 6 2.2 181 2 C95114 MutT/nudix family  
 279 6 2.2 181 2 D97983 conserved hypothet  
 280 6 2.2 181 2 G71171 hypothetical prote  
 281 6 2.2 185 2 AC3277 acetyltransferase  
 282 6 2.2 186 2 T29117 hypothetical prote  
 283 6 2.2 187 2 F69583 alkyl hydroperoxid  
 284 6 2.2 188 2 C96593 unknown protein, 9  
 285 6 2.2 189 2 T02792 hypothetical prote  
 286 6 2.2 189 2 F82969 hypothetical prote  
 287 6 2.2 191 2 G87253 hypothetical prote  
 288 6 2.2 193 2 S37139 phenylalanine-tRNA  
 289 6 2.2 194 2 AE2577 dephospho-CoA kina  
 290 6 2.2 194 2 D97359 hypothetical prote  
 291 6 2.2 194 2 T18336 icmC protein - Leg  
 292 6 2.2 194 2 F97209 probable membrane  
 293 6 2.2 195 2 G86683 prophage pil prote  
 294 6 2.2 195 2 D90415 hypothetical prote  
 295 6 2.2 196 2 A86690 prophage ps2 prote  
 296 6 2.2 196 2 D84074 hypothetical prote  
 297 6 2.2 197 2 AF0446 probable inhibitor  
 298 6 2.2 200 2 AC0343 probable CDP-alcoh  
 299 6 2.2 200 2 T40669 probable transcrip  
 300 6 2.2 201 2 AH0288 glutathione transf  
 301 6 2.2 201 2 D82896 hypothetical prote  
 302 6 2.2 201 2 H82055 peptidyl-prolyl ci  
 303 6 2.2 206 2 D83597 hypothetical prote  
 304 6 2.2 209 2 AC0273 probable exported  
 305 6 2.2 210 2 F71308 probable 2-dehydro  
 306 6 2.2 211 2 D71306 probable adenylate  
 307 6 2.2 211 2 S45464 hypothetical prote  
 308 6 2.2 215 2 A95879 probable dihydroxy  
 309 6 2.2 216 1 C41316 flagellin B2 precu  
 310 6 2.2 216 2 C83597 transforming prote  
 311 6 2.2 217 2 C70533 probable lexA prot  
 312 6 2.2 218 1 B41316 flagellin B1 precu  
 313 6 2.2 218 2 B47712 myelin/oligodendro  
 314 6 2.2 219 2 B72662 hypothetical prote  
 315 6 2.2 220 2 B84281 riboflavin-specifi  
 316 6 2.2 220 2 JH0425 GTP-binding protei  
 317 6 2.2 220 2 F72415 response regulator  
 318 6 2.2 220 2 D71677 hypothetical prote  
 319 6 2.2 221 2 G70533 probable phoYi pro  
 320 6 2.2 222 2 S19931 glycine-rich prote  
 321 6 2.2 223 1 S72693 dethiobiotin synth

322 6 2.2 224 2 E83522 conserved hypothet  
 323 6 2.2 225 2 F84171 hypothetical prote  
 324 6 2.2 225 2 F71439 probable serine pr  
 325 6 2.2 226 2 B75270 ABC transporter, A  
 326 6 2.2 226 2 D87061 dethiobiotin synth  
 327 6 2.2 227 2 T15035 adenosylhomocyste  
 328 6 2.2 228 2 F75493 hypothetical prote  
 329 6 2.2 228 2 T49891 glycine-rich prote  
 330 6 2.2 229 2 S73259 ribosomal protein  
 331 6 2.2 229 2 E87328 ribosomal protein  
 332 6 2.2 229 2 A97287 ribosomal protein  
 333 6 2.2 229 2 AD3487 acylpyruvate hydro  
 334 6 2.2 231 1 S74852 orotidine 5' monop  
 335 6 2.2 233 2 AB3468 glycine betaine/l-  
 336 6 2.2 233 2 T30747 hypothetical prote  
 337 6 2.2 234 2 A84253 chemotaxis protein  
 338 6 2.2 235 2 S72946 lexA protein - Myc  
 339 6 2.2 235 2 E95876 conserved hypothet  
 340 6 2.2 236 2 A90190 hypothetical prote  
 341 6 2.2 236 2 B96786 protein F10A5.19 [  
 342 6 2.2 238 1 D69930 probable 3-oxoacyl  
 343 6 2.2 238 2 F71723 ribosomal protein  
 344 6 2.2 238 2 D71189 hypothetical prote  
 345 6 2.2 239 2 B97722 50S ribosomal prot  
 346 6 2.2 240 2 S77496 ribosomal protein  
 347 6 2.2 240 2 G83208 conserved hypothet  
 348 6 2.2 240 2 H98031 hypothetical prote  
 349 6 2.2 241 1 S06998 acetoacetyl-CoA re  
 350 6 2.2 241 2 T17860 hypothetical prote  
 351 6 2.2 242 2 C83882 phosphoesterase-re  
 352 6 2.2 242 2 H86858 tRNA (Guanosine-2,  
 353 6 2.2 244 1 B42147 3-oxoacyl-[acyl]-ca  
 354 6 2.2 244 1 H64806 ybG1 protein - Esc  
 355 6 2.2 244 2 G90812 3-oxoacyl-[acyl]-ca  
 356 6 2.2 244 2 C85672 3-oxoacyl-[acyl]-ca  
 357 6 2.2 244 2 AD0642 3-oxoacyl-[acyl]-ca  
 358 6 2.2 244 2 B95166 ABC transporter, A  
 359 6 2.2 244 2 B90721 probable lactam ut  
 360 6 2.2 244 2 H85571 conserved hypothet  
 361 6 2.2 244 2 AF0588 hypothetical prote  
 362 6 2.2 244 2 S48482 hypothetical prote  
 363 6 2.2 244 2 C75605 protein F53C3.4 [i  
 364 6 2.2 245 1 VHUVUV nucleocapsid prote  
 365 6 2.2 245 2 S29580 class II histocomp  
 366 6 2.2 245 2 C65206 thif protein - Esc  
 367 6 2.2 245 2 C91243 thiamin biosynthes  
 368 6 2.2 245 2 A86091 thiamin biosynthes  
 369 6 2.2 245 2 E70583 hypothetical prote  
 370 6 2.2 245 2 G81297 hypothetical prote  
 371 6 2.2 245 2 C86418 3-oxoacyl-[acyl]-ca  
 372 6 2.2 246 2 H84136 polyketide synthas  
 373 6 2.2 246 2 JC5856 3-oxoacyl-[acyl]-ca  
 374 6 2.2 246 2 H72219 3-oxoacyl-[acyl]-ca  
 375 6 2.2 247 2 S77280 3-oxoacyl-[acyl]-ca  
 376 6 2.2 247 2 F65074 hypothetical oxido  
 377 6 2.2 247 2 D75027 dihydroorotate deh  
 378 6 2.2 248 2 H86527 oxoacyl (carrier p  
 379 6 2.2 248 2 G83253 probable short-cha  
 380 6 2.2 248 2 D72096 3-oxoacyl-[acyl]-ca  
 381 6 2.2 248 2 B21972 hypothetical prote  
 382 6 2.2 249 1 A31841 oxidoreductase, sh  
 383 6 2.2 249 2 B96022 probable dehydroge  
 384 6 2.2 249 2 A13573 3-oxoacyl-[acyl]-ca  
 385 6 2.2 249 2 AD2180 undecaprenyl pyrop  
 386 6 2.2 249 2 T11972 hypothetical prote  
 387 6 2.2 250 2 E82477 oxidoreductase, sh  
 388 6 2.2 250 2 C83622 probable short-cha  
 389 6 2.2 250 2 A70554 probable dehydroge  
 390 6 2.2 251 2 G72389 oxidoreductase, sh  
 391 6 2.2 251 2 D69848 3-oxoacyl-[acyl]-ca  
 392 6 2.2 251 2 AH2042 3-oxoacyl-[acyl]-ca  
 393 6 2.2 251 2 T15495 hypothetical prote

395	6	2.2	252	2	D83766	3-oxoacyl-(acyl)-ca	468	2	2.2	268	2	AI2237	septum site-determ
396	6	2.2	252	2	F83098	probable short-cha	469	6	2.2	268	2	B64780	probable transport
397	6	2.2	252	2	H75123	thiamin biosynthet	470	6	2.2	268	2	B90698	probable metal res
398	6	2.2	252	2	AU0932	thiamin biosynthes	471	6	2.2	268	2	D85548	probable metal res
399	6	2.2	252	2	AI1985	HesA protein (impo	472	6	2.2	269	2	E82472	hypothetical prote
400	6	2.2	252	2	F72560	hypothetical prote	473	6	2.2	269	2	AE2285	glucose 1-dehydrag
401	6	2.2	252	2	H96965	short-chain dehydr	474	6	2.2	269	2	F97308	periplasmic amino
402	6	2.2	253	2	C85067	2-deoxy-D-gluconat	475	6	2.2	269	2	H74420	phosphate transpor
403	6	2.2	253	2	C91091	2-deoxy-D-gluconat	476	6	2.2	269	2	H71889	phosphomethylpyrim
404	6	2.2	253	2	B83332	cis-1,2-dihydroxyc	477	6	2.2	270	2	T00667	3-oxoacyl-(acyl)-ca
405	6	2.2	253	2	F83134	probable short-cha	478	6	2.2	270	2	S47479	outer surface prot
406	6	2.2	253	2	F85936	2-deoxy-D-gluconat	479	6	2.2	270	2	D64625	outer surface prot
407	6	2.2	253	2	B95284	probable (imported	480	6	2.2	272	2	E70879	thiamin biosynthes
408	6	2.2	253	2	AC0868	2-keto-3-deoxygluc	481	6	2.2	272	2	E70879	probable dehydroge
409	6	2.2	253	2	T27951	hypothetical prote	482	6	2.2	273	2	A97281	hydroxyethylthazo
410	6	2.2	253	2	T02106	hypothetical prote	483	6	2.2	273	2	S71541	outer surface prot
411	6	2.2	254	2	C70387	dehydrogenase - Ag	484	6	2.2	273	2	S71544	outer surface prot
412	6	2.2	254	2	S48129	3(or 17)beta-hydro	485	6	2.2	273	2	I40102	outer surface prot
413	6	2.2	254	2	AC3256	3-oxoacyl-(acyl)-ca	486	6	2.2	273	2	I40099	outer surface prot
414	6	2.2	254	2	AD3182	short chain dehydr	487	6	2.2	273	2	I40097	outer surface prot
415	6	2.2	254	2	S76645	hypothetical prote	488	6	2.2	273	2	I40139	outer surface prot
416	6	2.2	254	2	H69057	hypothetical prote	489	6	2.2	273	2	S71531	outer surface prot
417	6	2.2	254	2	C75540	probable histidine	490	6	2.2	273	2	S71531	outer surface prot
418	6	2.2	255	2	T39164	serbitol utilization	491	6	2.2	274	2	B72227	nicotinate-nucleot
419	6	2.2	255	2	T71007	thiamin biosynthes	492	6	2.2	274	2	A64385	transketolase (EC
420	6	2.2	256	2	E72427	oxidoreductase, sh	493	6	2.2	275	2	B70640	hypothetical prote
421	6	2.2	256	2	D84201	enoyl-CoA hydratase	494	6	2.2	275	2	T01088	hypophan synthase
422	6	2.2	256	2	D87711	molybdopterin bios	495	6	2.2	276	2	D70953	hypothetical prote
423	6	2.2	257	2	D83280	probable short-cha	496	6	2.2	277	2	A43890	fdxH 5'-region hyp
424	6	2.2	257	2	T35593	probable dehydroge	497	6	2.2	277	2	S40167	hypothetical prote
425	6	2.2	257	2	D97152	uncharacterized se	498	6	2.2	277	2	S76356	proteinase IV (EC
426	6	2.2	257	2	T18754	hypothetical prote	499	6	2.2	277	2	E70878	hypothetical prote
427	6	2.2	258	2	T20484	hypothetical prote	500	6	2.2	278	1	SO1065	glutamine amidotra
428	6	2.2	258	2	T36264	probable dehydroge	501	6	2.2	278	1	AC0356	probable dehydroge
429	6	2.2	258	2	T09786	expansin - upland	502	6	2.2	279	2	D86658	probable RpiR-fami
430	6	2.2	258	2	B83220	ferredoxin-NADP+ r	503	6	2.2	281	2	D86658	oxidoreductase ycg
431	6	2.2	258	2	AC5732	ferredoxin-NADP re	504	6	2.2	281	2	F97844	hypothetical prote
432	6	2.2	259	2	E55217	cis-1,2-dihydro-1,	505	6	2.2	281	2	AI3196	transcription regu
433	6	2.2	259	2	D49343	cis-1,2-dihydro-1,	506	6	2.2	281	2	T01445	hypothetical prote
434	6	2.2	259	2	AE3185	dehydrogenase Atu5	507	6	2.2	282	1	JC4041	D-arabinitol 2-deh
435	6	2.2	259	2	AB0565	probable membrane	508	6	2.2	282	2	T37144	probable oxidoredu
436	6	2.2	259	2	AD2926	conserved hypoteth	509	6	2.2	282	2	D72771	probable bacterioc
437	6	2.2	259	2	C98356	hypothetical prote	510	6	2.2	283	2	S53941	hypothetical prote
438	6	2.2	260	2	H87264	3-hydroxyacyl-CoA	511	6	2.2	284	2	T33860	hypothetical prote
439	6	2.2	260	2	H70758	probable fabG3 pro	512	6	2.2	285	2	T50932	short-chain dehydr
440	6	2.2	260	2	D60004	probable 3-oxoacyl	513	6	2.2	285	2	D69835	alcohol dehydrogen
441	6	2.2	261	2	T38157	short-chain dehydr	514	6	2.2	285	2	T51576	hypothetical prote
442	6	2.2	261	2	AD2895	short-chain dehydr	515	6	2.2	286	1	A71090	hypothetical prote
443	6	2.2	261	2	G97670	probable oxidoredu	516	6	2.2	286	2	A70667	hypothetical prote
444	6	2.2	262	2	G84694	probable tropinone	517	6	2.2	286	2	AI3207	NAD/NADP dependant
445	6	2.2	262	2	T31253	1,6-dihydroxycyclo	518	6	2.2	287	2	AG5193	dehydrogenase Atu5
446	6	2.2	262	2	F87498	exodeoxyribonuclea	519	6	2.2	287	2	AF2716	conserved hypoteth
447	6	2.2	262	2	AD0164	conserved hypoteth	520	6	2.2	288	2	S74895	hypothetical prote
448	6	2.2	263	2	S73266	ribosomal protein	521	6	2.2	289	2	T48108	hypothetical prote
449	6	2.2	263	2	B83751	N-acetylglucosamin	522	6	2.2	290	1	D81738	probable 3',5'-cyc
450	6	2.2	263	2	A75280	phenylacetic acid	523	6	2.2	292	2	F71901	hypothetical prote
451	6	2.2	263	2	G97198	HAD superfamily hy	524	6	2.2	292	2	E64614	beta-alanine synth
452	6	2.2	264	2	T30224	3-oxoacyl-(acyl) ca	525	6	2.2	293	2	S35983	proline transport
453	6	2.2	264	2	S60874	phosphorylation-ac	526	6	2.2	293	2	C90032	hypothetical prote
454	6	2.2	264	2	F96832	hypothetical prote	527	6	2.2	293	2	T36063	probable integral
455	6	2.2	264	2	B72411	conserved hypoteth	528	6	2.2	293	2	C71703	hypothetical prote
456	6	2.2	265	1	WPBBG7	gene 7 protein - p	529	6	2.2	294	2	AE1517	oxidoreductase hom
457	6	2.2	265	2	T33294	hypothetical prote	530	6	2.2	294	2	AE1158	probable short-cha
458	6	2.2	265	2	S70247	hypothetical prote	531	6	2.2	295	2	H83452	3-oxoacyl-(acyl)-ca
459	6	2.2	265	2	AE0455	thiamin biosynthes	532	6	2.2	297	2	T51084	probable oxidoredu
460	6	2.2	265	2	AE2964	transcription regu	533	6	2.2	297	2	S19842	oxidoreductase Atu
461	6	2.2	265	2	H98318	hypothetical prote	534	6	2.2	297	2	AI3125	probable oxidoredu
462	6	2.2	266	2	T31264	cis-1,2-dihydro-1,	535	6	2.2	298	2	AF4089	probable oxidoredu
463	6	2.2	266	2	S76970	hypothetical prote	536	6	2.2	298	2	AF3578	transporter dme f
464	6	2.2	266	2	S11900	hypothetical prote	537	6	2.2	299	2	D81399	malate dehydrogena
465	6	2.2	267	1	F64103	suppressor protein	538	6	2.2	300	2	C70586	probable bex - hyc
466	6	2.2	268	2	AD2604	oxidoreductase Xf2	539	6	2.2	300	2	AC1597	integrase/recombin
467	6	2.2	268	2	G96016	probable gluconate	540	6	2.2	300	2	AE1234	integrase/recombin

541	6	2.2	300	2	F81331	hypothetical prote	614	2	I39563	probable UDPglucos
542	6	2.2	302	2	A86898	phosphogluconate d	615	2	AB2772	inosine-uridine pr
543	6	2.2	302	2	T03575	conserved hypothet	616	2	S48698	3-dehydroquinatate d
544	6	2.2	302	2	AH1749	transcription regu	617	6	C95952	hypothetical prote
545	6	2.2	302	2	D70538	probable bpob prot	618	6	B82301	conserved hypothet
546	6	2.2	303	2	H97034	cysteine synthase	619	6	G96812	protein F3P9.6 lim
547	6	2.2	304	2	F84298	hypothetical prote	620	6	YWBSF	tryptophan-tRNA li
548	6	2.2	304	2	T48281	hypothetical prote	621	6	F90675	probable sugar-bin
549	6	2.2	305	2	E89771	lipoprotein [impor	622	6	A85526	probable sugar-bin
550	6	2.2	306	2	S60670	ParA-like partitio	623	6	D71887	ADPglyceromanno-he
551	6	2.2	307	2	D75070	dipeptidase PA8238	624	6	YWBS	tryptophan-tRNA li
552	6	2.2	307	2	G89501	UDP-glucose 4-epim	625	6	C64827	ADPglyceromanno-he
553	6	2.2	308	2	D83452	probable cytochrom	626	6	F84008	tryptophanyl-tRNA
554	6	2.2	308	2	A86378	protein F21J9.2 [i	627	6	A82510	conserved hypothet
555	6	2.2	308	2	S67657	hypothetical prote	628	6	AG3650	succinoglycan bios
556	6	2.2	308	2	G98161	hypothetical oxido	629	6	AF1349	tryptophanyl-tRNA
557	6	2.2	308	2	AF2890	transcription regu	630	6	AI1719	tryptophanyl-tRNA
558	6	2.2	308	2	B97666	probable transcrip	631	6	A99605	hypothetical prote
559	6	2.2	308	2	D70875	probable PE protei	632	6	A70388	hydrogenase expre
560	6	2.2	308	2	T08798	hypothetical prote	633	6	T39657	hypothetical prote
561	6	2.2	309	2	C83136	probable epimerase	634	6	A57140	motB protein homol
562	6	2.2	309	2	B86702	Hpr(Ser) kinase [i	635	6	A49338	phosphate acetyltr
563	6	2.2	309	2	F72316	hypothetical prote	636	6	F69495	conserved hypothet
564	6	2.2	309	2	A83325	comL, competence l	637	6	T05230	hypothetical prote
565	6	2.2	309	2	S67196	probable membrane	638	6	AB1965	tryptophanyl-tRNA
566	6	2.2	310	1	G70330	ADPglyceromanno-he	639	6	AF3309	moxR protein [impo
567	6	2.2	310	2	S45919	hypothetical prote	640	6	T26160	hypothetical prote
568	6	2.2	311	1	A64623	thioredoxin-diulf	641	6	G83207	hypothetical prote
569	6	2.2	311	2	T37155	probable oxidoredu	642	6	AE2922	zinc-binding dehyd
570	6	2.2	311	2	D71890	thioredoxin reduct	643	6	F97696	hypothetical zinc-
571	6	2.2	311	2	A87527	ornithine carbamoy	644	6	A47542	short-chain alcohoh
572	6	2.2	311	2	T21206	hypothetical prote	645	6	H75255	oxidoreductase, sh
573	6	2.2	311	2	AP2810	transcription regu	646	6	T41543	probable cell cycl
574	6	2.2	313	2	C86651	UDP-glucose 4-epim	647	6	S77630	hypothetical prote
575	6	2.2	313	2	C81288	probable sugar-nuc	648	6	TVMSFB	transforming prote
576	6	2.2	314	2	B70569	hypothetical prote	649	6	S48299	SAS2 protein - yea
577	6	2.2	314	2	G86515	oligopeptide perme	650	6	S73775	lipotease protein li
578	6	2.2	314	2	E72107	peptide ABC transp	651	6	G82545	phage-related inte
579	6	2.2	314	2	D87576	oxidoreductase, al	652	6	AF2018	hypothetical prote
580	6	2.2	314	2	A87693	transcription regu	653	6	F75557	oxidoreductase, sh
581	6	2.2	314	2	S15311	hypothetical prote	654	6	D72025	flagellar m-ring p
582	6	2.2	314	2	AI0765	probable rhamnosyl	655	6	B86598	flagellar M-ring p
583	6	2.2	315	1	S73917	thioredoxin-diulf	656	6	AG2772	NADPH:quinone redu
584	6	2.2	315	2	S39727	dtDPglucose 4,6-de	657	6	E97552	alcohol dehydrogen
585	6	2.2	315	2	G96997	nucleoside-diphosp	658	6	S60386	hypothetical prote
586	6	2.2	315	2	E71729	proteinase DO (htr	659	6	T41498	DNA (apurinic or a
587	6	2.2	315	2	T00528	hypothetical prote	660	6	T22541	hypothetical prote
588	6	2.2	316	1	S27981	homoserine kinase	661	6	A98182	transcription regu
589	6	2.2	316	1	A42935	N-acetylmuramoyl-L	662	6	AB3105	transcription regu
590	6	2.2	316	2	A38265	peroxidase (EC 1.1	663	6	S52817	electron transfer
591	6	2.2	316	2	H82958	homoserine kinase	664	6	PC4185	hemagglutinin 1 ch
592	6	2.2	317	1	S67781	probable membrane	665	6	B71296	probable sn-1,2-di
593	6	2.2	317	2	C86479	probable annexin p	666	6	S36080	hemagglutinin - in
594	6	2.2	318	2	E90541	hypothetical prote	667	6	JQ1908	hemagglutinin 1 -
595	6	2.2	318	2	G84196	cation antiporter	668	6	JQ1909	hemagglutinin 1 -
596	6	2.2	319	1	S56523	dihydrodipicolinat	669	6	JQ1913	hemagglutinin 1 -
597	6	2.2	319	2	S22416	3-oxoacyl-[acyl-ca	670	6	JQ1906	hemagglutinin 1 -
598	6	2.2	319	2	C89859	hypothetical prote	671	6	JQ1915	hemagglutinin 1 -
599	6	2.2	319	2	D71633	[acyl-carrier-prot	672	6	JQ1916	hemagglutinin 1 -
600	6	2.2	319	2	A97589	transcription regu	673	6	JQ1911	hemagglutinin 1 -
601	6	2.2	320	2	S22450	3-oxoacyl-[acyl-ca	674	6	JQ1914	hemagglutinin 1 -
602	6	2.2	320	2	AD1317	asparaginase homol	675	6	JQ1912	hemagglutinin 1 -
603	6	2.2	320	2	AD1689	asparaginase homol	676	6	JQ1907	hemagglutinin 1 -
604	6	2.2	320	2	B99254	formate hydrogenly	677	6	JQ1910	hemagglutinin 1 -
605	6	2.2	321	2	G95920	probable epimerase	678	6	S60428	hypothetical prote
606	6	2.2	322	2	S18999	asparaginase (EC 3	679	6	D84653	probable tryptophan
607	6	2.2	322	2	JN0265	genome polyprotein	680	6	F87440	rod shape-determin
608	6	2.2	322	2	A64470	NADH dehydrogenase	681	6	JQ1901	hemagglutinin 1 -
609	6	2.2	323	2	T52563	probable DNA-(apur	682	6	JQ1904	hemagglutinin 1 -
610	6	2.2	323	2	H71968	delta-aminolevulin	683	6	JQ1902	hemagglutinin 1 -
611	6	2.2	323	2	D89773	hypothetical prote	684	6	JQ1905	hemagglutinin 1 -
612	6	2.2	323	2	B48067	ethanolamine-phosp	685	6	JQ1903	hemagglutinin 1 -
613	6	2.2	323	2	D72661	hypothetical prote	686	6	S64041	probable membrane

687	6	2.2	348	2	A70311	hypothetical prote	760	6	2.2	380	2	S78342	hypothetical prote
688	6	2.2	349	2	T41497	DNA (apurinic or a	761	6	2.2	380	2	G69604	spore coat protein
689	6	2.2	349	2	F95887	probable ABC trans	762	6	2.2	381	1	A42952	methanol dehydrog
690	6	2.2	349	2	A72605	probable high-affi	763	6	2.2	382	2	T11138	ubiquinol-cytochro
691	6	2.2	350	2	G75212	hypothetical prote	764	6	2.2	382	2	T49077	hypothetical prote
692	6	2.2	351	2	A81393	threonine synthase	765	6	2.2	382	2	T24963	hypothetical prote
693	6	2.2	351	2	A81768	threonine synthase	766	6	2.2	383	2	AG3229	NAD/NADP octopine/
694	6	2.2	351	2	A84827	hypothetical prote	767	6	2.2	384	2	S77238	hypothetical prote
695	6	2.2	351	2	F92880	hypothetical ferri	768	6	2.2	384	2	D75638	probable coenzyme
696	6	2.2	351	2	HN1878	hemagglutinin prec	769	6	2.2	385	2	A44102	di-N-acetylchitobi
697	6	2.2	353	2	C54187	outer membrane pro	770	6	2.2	387	2	T09086	sedoheptulose-bisp
698	6	2.2	353	2	H83482	hypothetical prote	771	6	2.2	387	2	T23887	hypothetical prote
699	6	2.2	353	2	H69855	hypothetical prote	772	6	2.2	387	2	AE2750	hypothetical prote
700	6	2.2	353	2	S50086	finger protein xpo	773	6	2.2	387	2	D97431	ubiquinol-cytochro
701	6	2.2	354	1	S73697	probable X-Pro dip	774	6	2.2	388	1	CBZM	xylose isomerase (
702	6	2.2	354	2	F43225	aspartate-semialde	775	6	2.2	388	1	E41339	xylose isomerase (
703	6	2.2	354	2	S46245	RAE-30 protein - m	776	6	2.2	388	2	JC1031	myosin heavy chain
704	6	2.2	355	2	G65182	dtDP-glucose 4,6-de	777	6	2.2	389	2	S01371	RNA helicase BH334
705	6	2.2	355	2	A31219	dtDP-glucose 4,6-d	778	6	2.2	389	2	D84068	hypothetical prote
706	6	2.2	355	2	C86065	dtDP-glucose 4,6-d	779	6	2.2	389	2	F86212	hypothetical prote
707	6	2.2	355	2	C751134	x-pro aminopeptida	780	6	2.2	390	2	G75591	oxidoreductase, sh
708	6	2.2	355	2	D97139	dioxygenase relate	781	6	2.2	391	2	T41849	ACMNPV orf109 - Bo
709	6	2.2	356	2	A81811	dtDP-glucose 4-6-d	782	6	2.2	391	2	A95979	probable sugar upt
710	6	2.2	356	2	C97158	aminopeptidase P A	783	6	2.2	392	1	CBVF	ubiquinol-cytochro
711	6	2.2	356	2	A95361	probable transcrip	784	6	2.2	392	2	T36967	probable geranylge
712	6	2.2	357	2	A83139	zinc-binding dehyd	785	6	2.2	393	1	S38960	ubiquinol-cytochro
713	6	2.2	357	2	T08642	hypothetical prote	786	6	2.2	393	1	CBPOM	ubiquinol-cytochro
714	6	2.2	357	2	H65041	hypothetical prote	787	6	2.2	393	2	G71173	hypothetical prote
715	6	2.2	358	2	T05081	fructose-bisphosph	788	6	2.2	394	1	CBOBE	ubiquinol-cytochro
716	6	2.2	359	2	S83355	hypothetical prote	789	6	2.2	395	2	F81343	ubiquinol-cytochro
717	6	2.2	360	2	D93025	hypothetical prote	790	6	2.2	395	2	S70912	CMP-N-acetylneuram
718	6	2.2	361	2	S45299	pleiotropic regula	791	6	2.2	396	2	T11381	hypothetical prote
719	6	2.2	361	2	A07667	dtDP-glucose 4,6-de	792	6	2.2	397	2	CBRZ	ubiquinol-cytochro
720	6	2.2	361	2	G26636	dtDP-glucose 4,6-d	793	6	2.2	397	2	T14263	ubiquinol-cytochro
721	6	2.2	362	2	A86393	TiK7.4 protein - A	794	6	2.2	397	2	S98148	(R,R)-butanediol d
722	6	2.2	362	2	E83542	hypothetical prote	795	6	2.2	397	2	A30091	caps protein - Bac
723	6	2.2	363	2	A33609	hypothetical prote	796	6	2.2	398	1	A22931	ubiquinol-cytochro
724	6	2.2	363	2	A33609	ABC transporter su	797	6	2.2	398	2	T49098	hypothetical prote
725	6	2.2	364	2	T45253	probable antiporte	798	6	2.2	398	2	T08716	uracil permease -
726	6	2.2	365	2	A83363	membrane fusion pr	799	6	2.2	399	2	F72329	hypothetical prote
727	6	2.2	365	1	AJFF32C	glutamate-ammonia	800	6	2.2	399	2	D86322	conserved hypothet
728	6	2.2	365	2	A02090	NADH flavin oxidor	801	6	2.2	399	2	A95200	hypothetical prote
729	6	2.2	366	2	G82069	conserved hypothet	802	6	2.2	399	2	H80666	hypothetical prote
730	6	2.2	367	2	JC6138	extracellular sign	803	6	2.2	400	2	B69081	acetyl-CoA synthet
731	6	2.2	367	2	JC5252	mitogen-activated	804	6	2.2	401	2	A81335	tyrosine-tRNA liga
732	6	2.2	367	2	B84169	molybdenum cofacto	805	6	2.2	401	2	T17500	major capsid-like
733	6	2.2	368	2	E71204	hypothetical prote	806	6	2.2	402	2	A35741	renin-binding prot
734	6	2.2	369	2	T45021	hypothetical prote	807	6	2.2	402	2	D72400	hypothetical prote
735	6	2.2	371	2	A87322	Protein-Glutamate	808	6	2.2	402	2	T15677	hypothetical prote
736	6	2.2	372	2	F01500	Pentapeptide repea	809	6	2.2	404	1	S62440	mevalonate kinase
737	6	2.2	372	2	S67770	mannose-6-phosphat	810	6	2.2	404	2	T36254	probable valine-by
738	6	2.2	373	2	B95871	probable membrane	811	6	2.2	405	1	JH0795	calreticulin precu
739	6	2.2	373	2	A70334	probable CUP-tyvel	812	6	2.2	405	2	H64482	threonine synthase
740	6	2.2	374	2	D83328	hypothetical prote	813	6	2.2	405	2	F97340	probable flavoprot
741	6	2.2	374	2	JC2124	probable aminotran	814	6	2.2	405	2	S23260	hypothetical prote
742	6	2.2	374	2	JC2123	major allergen Cry	815	6	2.2	406	2	H64925	aminotransferase n
743	6	2.2	374	2	B86198	major allergen Cry	816	6	2.2	406	2	C90927	selenocysteine lya
744	6	2.2	374	2	C75018	hypothetical prote	817	6	2.2	406	2	G85775	selenocysteine lya
745	6	2.2	375	2	AC0484	hypothetical prote	818	6	2.2	406	2	AG0702	probable aminotran
746	6	2.2	375	2	B83954	probable regulator	819	6	2.2	406	2	T39786	hypothetical prote
747	6	2.2	376	2	A45634	flagella-associate	820	6	2.2	407	2	C64250	tyrosine-tRNA liga
748	6	2.2	376	2	S47051	actin - Cryptospor	821	6	2.2	408	2	T46063	glutamate permease
749	6	2.2	377	1	D69027	hypothetical prote	822	6	2.2	409	2	B64708	hypothetical prote
750	6	2.2	377	2	S77142	conserved hypothet	823	6	2.2	409	2	B95372	probable integrase
751	6	2.2	377	2	F69122	tryptophan-tRNA li	824	6	2.2	409	2	F95409	probable integrase
752	6	2.2	377	2	T45784	conserved hypothet	825	6	2.2	410	2	T25165	hypothetical prote
753	6	2.2	377	2	S36081	hypothetical prote	826	6	2.2	411	2	AE3052	two component sens
754	6	2.2	378	2	S11738	probable carrier p	827	6	2.2	412	2	G64685	hypothetical prote
755	6	2.2	378	2	A97552	hemagglutinin prec	828	6	2.2	413	2	H66885	ammonium transport
756	6	2.2	378	2	AC0646	chain a, crystal s	829	6	2.2	414	2	G82705	conserved hypothet
757	6	2.2	378	2	AC0646	spermidine/putresc	830	6	2.2	414	2	C83544	probable MFS trans
758	6	2.2	379	2	JN00104	hypothetical prote	831	6	2.2	416	2	S09334	transcobalamin i p
759	6	2.2	379	2	B95883	synaptic vesicle m	832	6	2.2	417	2	F70132	conserved hypothet

833	6	2.2	417	2	JX0188	renin-binding prot	906	6	2.2	472	2	F81208
834	6	2.2	417	2	B40016	matrin 3 - human (	907	6	2.2	472	2	H96607
835	6	2.2	417	2	F98233	two-component sens	908	6	2.2	474	2	T44424
836	6	2.2	418	2	D83902	maltose/maltodextr	909	6	2.2	474	2	S30227
837	6	2.2	419	2	JX0187	renin-binding prot	910	6	2.2	475	2	C97684
838	6	2.2	419	2	A36509	N-acyleuraminat	911	6	2.2	476	2	S12461
839	6	2.2	419	2	S53374	mannanase A - pseu	912	6	2.2	476	2	A40469
840	6	2.2	419	2	D82408	conserved hypothet	913	6	2.2	476	2	S09489
841	6	2.2	421	2	C70038	maltose/maltodextr	914	6	2.2	476	2	F87324
842	6	2.2	421	2	E83038	probable heat-shoc	915	6	2.2	477	2	S16383
843	6	2.2	421	2	T19203	hypothetical prote	916	6	2.2	477	2	H83389
844	6	2.2	423	2	E84751	hypothetical prote	917	6	2.2	478	2	A45796
845	6	2.2	425	2	G75414	seryl-tRNA synthet	918	6	2.2	478	2	A83449
846	6	2.2	426	2	C97377	tetrahydrofolylpol	919	6	2.2	479	2	A48565
847	6	2.2	427	2	T29376	hypothetical prote	920	6	2.2	479	2	T29720
848	6	2.2	427	2	A11491	permeases homolog	921	6	2.2	480	2	F86207
849	6	2.2	429	2	F71651	putrescine-ornithi	922	6	2.2	480	2	H70854
850	6	2.2	429	2	T40112	3-hydroxyisobutyry	923	6	2.2	481	2	S69808
851	6	2.2	432	2	A12613	hypothetical prote	924	6	2.2	481	2	T33733
852	6	2.2	432	2	G97395	hypothetical prote	925	6	2.2	483	2	T52136
853	6	2.2	432	2	B75638	hypothetical prote	926	6	2.2	483	2	D87543
854	6	2.2	433	1	A34227	transcobalamin I p	927	6	2.2	484	2	H64105
855	6	2.2	433	2	T46528	probable CDP-4-ket	928	6	2.2	484	2	T26393
856	6	2.2	433	2	G71657	folypolyglutamate	929	6	2.2	485	2	B82558
857	6	2.2	433	2	C83271	conserved hypothet	930	6	2.2	485	2	H87463
858	6	2.2	438	2	A83544	probable transport	931	6	2.2	488	2	A72554
859	6	2.2	438	2	G87337	membrane protein,	932	6	2.2	489	2	B72518
860	6	2.2	440	2	A21395	conserved hypothet	933	6	2.2	490	1	C57150
861	6	2.2	440	2	A11770	conserved hypothet	934	6	2.2	492	2	T38211
862	6	2.2	441	2	T22531	hypothetical prote	935	6	2.2	493	2	A83581
863	6	2.2	441	2	C64026	hypothetical prote	936	6	2.2	493	2	A97439
864	6	2.2	441	2	E84264	isochorismate synt	937	6	2.2	493	2	AD2657
865	6	2.2	441	2	T34032	hypothetical prote	938	6	2.2	496	2	C83122
866	6	2.2	445	2	S73966	MG148 homolog Vxps	939	6	2.2	496	2	D75293
867	6	2.2	447	2	S66256	alpha-1,6-mannosyl	940	6	2.2	497	2	JC4524
868	6	2.2	447	2	C75413	probable proteinase	941	6	2.2	497	2	B97729
869	6	2.2	448	2	G95416	probable response	942	6	2.2	497	2	A96828
870	6	2.2	453	2	S52690	hypothetical prote	943	6	2.2	498	2	H69623
871	6	2.2	453	2	H64974	hypothetical prote	944	6	2.2	499	2	D72342
872	6	2.2	453	2	A98990	hypothetical prote	945	6	2.2	499	2	S39113
873	6	2.2	453	2	D85835	hypothetical prote	946	6	2.2	500	1	ITHUC1
874	6	2.2	453	2	A80774	hypothetical prote	947	6	2.2	502	2	T35743
875	6	2.2	454	2	C82941	ATP synthase beta	948	6	2.2	503	2	T29870
876	6	2.2	454	2	I64124	virion morphogenes	949	6	2.2	503	2	S23243
877	6	2.2	454	2	H83377	probable transport	950	6	2.2	504	1	I49428
878	6	2.2	454	2	S16565	noli protein - Rhi	951	6	2.2	504	2	T49185
879	6	2.2	455	1	S08510	cruciferin precurs	952	6	2.2	505	2	E83918
880	6	2.2	455	2	E86169	12S seed storage p	953	6	2.2	506	2	T28810
881	6	2.2	455	2	E83598	signal recognition	954	6	2.2	506	2	T01716
882	6	2.2	456	2	AH0551	proline-specific p	955	6	2.2	506	2	F85016
883	6	2.2	456	2	B86834	sensor protein kin	956	6	2.2	506	2	B82043
884	6	2.2	457	2	B64769	proline transport	957	6	2.2	507	2	H69186
885	6	2.2	457	2	D90685	proline permease t	958	6	2.2	507	2	T32614
886	6	2.2	457	2	H85535	proline permease t	959	6	2.2	509	2	E90071
887	6	2.2	457	2	D82961	probable metallopr	960	6	2.2	510	1	S43692
888	6	2.2	457	2	B82945	chromosomal replic	961	6	2.2	512	2	B96785
889	6	2.2	457	2	S61974	SSU1 protein - yea	962	6	2.2	513	2	S08381
890	6	2.2	460	2	S35470	NADH2 dehydrogenas	963	6	2.2	514	2	A57280
891	6	2.2	461	1	S65187	GPI-anchor biosynt	964	6	2.2	515	2	E84577
892	6	2.2	462	2	B82510	transporter, Nadc	965	6	2.2	515	2	T40649
893	6	2.2	462	2	T27323	hypothetical prote	966	6	2.2	515	2	PC4419
894	6	2.2	462	2	I51699	gene XGP 5.1C prot	967	6	2.2	516	2	S34525
895	6	2.2	463	2	A10388	probable proline-s	968	6	2.2	516	2	TQ2389
896	6	2.2	463	2	S84119	hypothetical prote	969	6	2.2	516	2	T24729
897	6	2.2	464	2	T39699	glutathione-disulf	970	6	2.2	517	1	A40872
898	6	2.2	464	2	A75615	conserved hypothet	971	6	2.2	518	2	H97320
899	6	2.2	464	2	AD3639	zinc proteinase (E	972	6	2.2	518	2	T45765
900	6	2.2	465	1	S14762	cruciferin 4 precu	973	6	2.2	519	2	S60661
901	6	2.2	465	2	F82288	probable proteinase	974	6	2.2	519	2	T24772
902	6	2.2	467	2	A59288	modulation competi	975	6	2.2	520	2	T30808
903	6	2.2	467	2	T15892	hypothetical prote	976	6	2.2	522	2	D96913
904	6	2.2	468	2	I64182	Na+/H+-exchanging	977	6	2.2	523	2	T28721
905	6	2.2	469	2	AD2909	3-isopropylmalate	978	6	2.2	524	2	T09937
						glutamate-ammonia						
						unknown protein F2						
						dihydrolipoamide d						
						transposase - C1os						
						2-isopropylmalate						
						carboxypeptidase E						
						carboxypeptidase E						
						hypothetical prote						
						carboxypeptidase E						
						hypothetical prote						
						dihydrolipoamide d						
						phosphogluconate d						
						hypothetical prote						
						hypothetical prote						
						lincomycin resist						
						hypothetical prote						
						dihydrolipoamide S						
						methionyl-CoA						
						pantothenate trans						
						hypothetical prote						
						IMP dehydrogenase						
						hypothetical prote						
						probable Glu-tRNA						
						hypothetical prote						
						NADP-reducing hydr						
						hypothetical prote						
						probable c-type cy						
						phosphate permease						
						probable aldehyde						
						uracil permease -						
						aldenhyde dehydroge						
						heat shock protein						
						hypothetical prote						
						flagellar hook-ass						
						tldD protein - The						
						alpha-N-arabinofur						
						complement C1 inh						
						ribosomal protein						
						hypothetical prote						
						hypothetical prote						
						cytochrome P450 16						
						cytokinin oxidase-						
						carboxypeptidase B						
						hypothetical prote						
						hypothetical prote						
						probable RING zinc						
						conserved hypothet						
						hypothetical prote						
						zinc metalloprotei						
						transcription fact						
						hypothetical prote						
						keratin, 58K type						
						spindle pole body-						
						probable cytokinin						
						hypothetical prote						
						actin-binding 260K						
						hypothetical prote						
						sucrose transport						
						hypothetical prote						
						aldenhyde dehydroge						
						PTS system, (possi						
						hypothetical prote						
						legumin - welwisc						
						hypothetical prote						
						hypothetical prote						
						phosphatase, sulfate ad						
						hypothetical prote						
						cytokinin oxidase						

979 6 2.2 526 2 T47786  
 980 6 2.2 527 2 D84517  
 981 6 2.2 531 2 E83371  
 982 6 2.2 532 2 F84101  
 983 6 2.2 532 2 D82354  
 984 6 2.2 533 2 S62336  
 985 6 2.2 533 2 T04481  
 986 6 2.2 533 2 S47271  
 987 6 2.2 533 2 A0180  
 988 6 2.2 534 2 T5414  
 989 6 2.2 534 2 T01500  
 990 6 2.2 534 2 T51929  
 991 6 2.2 535 2 D84340  
 992 6 2.2 536 2 D83622  
 993 6 2.2 537 2 T04944  
 994 6 2.2 538 2 A83632  
 995 6 2.2 538 2 F83622  
 996 6 2.2 541 2 T13496  
 997 6 2.2 541 2 A71649  
 998 6 2.2 543 2 D83262  
 999 6 2.2 543 2 A28671  
 1000 6 2.2 544 2 S62527

ALIGNMENTS

RESULT 1  
 T03734  
 short chain alcohol dehydrogenase homolog - common tobacco  
 N:Alternate names: TFHP-1 protein  
 C:Species: Nicotiana tabacum (common tobacco)  
 C>Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 21-Jul-2000  
 C:Accession: T03734  
 R:Kawaoka, A.; Kawamoto, T.; Sekine, M.; Yoshida, K.; Takano, M.; Shimmyo, A.  
 Plant J. 6, 87-97, 1994  
 A>Title: A cis-acting element and a trans-acting factor involved in the wound-induced ex  
 A:Reference number: Z15039; MUID:95004656; PMID:7920706  
 A:Accession: T03734  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-234 <RAW>  
 A:Cross-references: EMBL:D29976; NID:G531268; PIDN:BA06241.1; PID:G531269  
 A:Experimental source: strain cv. Petite Havana SR-1  
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 6.2%; Score 17; DB 2; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 28-09;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 10 RLEGKVALITGGASGIG 26  
 Db 13 RLEGKVALITGGASGIG 29  
 RESULT 2  
 T02257  
 probable short chain alcohol dehydrogenase - common tobacco  
 C:Species: Nicotiana tabacum (common tobacco)  
 C>Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 21-Jul-2000  
 C:Accession: T02257  
 R:Herbers, K.; Moenke, G.; Badur, R.; Sonnenwald, U.  
 Plant Mol. Biol. 29, 1027-1038, 1995  
 A>Title: A simplified procedure for the subtractive cDNA cloning of photoassimilate-resp  
 A:Reference number: S62698; MUID:96145513; PMID:8555446  
 A:Accession: T02257  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-284 <HER>  
 A:Cross-references: EMBL:AJ223177; NID:G2739278; PIDN:CA11153.1; PID:G2739279  
 A:Experimental source: cultivar SNN; tissue-type leaf  
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 6.2%; Score 17; DB 2; Length 284;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-09;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 10 RLEGKVALITGGASGIG 26  
 Db 13 RLEGKVALITGGASGIG 29  
 RESULT 3  
 H85039  
 probable alcohol dehydrogenase [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 02-Mar-2001  
 C:Accession: H85039  
 R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring  
 Nature 402, 769-777, 1999  
 A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
 A:Reference number: A85001; MUID:20083488; PMID:10617198  
 A:Accession: H85039  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-283 <STO>  
 A:Cross-references: GB:NC\_001268; NID:G2720184; PIDN:CAB77799.1; GSPDB:GN00140  
 C:Genetics:  
 A:Gene: AT4G03140  
 A:Map position: 4  
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 5.9%; Score 16; DB 2; Length 283;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 11 LEGKVALITGGASGIG 26  
 Db 18 LEGKVALITGGASGIG 33  
 RESULT 4  
 T11579  
 probable short chain alcohol dehydrogenase CPRD12, drought-inducible - cowpea  
 C:Species: Vigna unguiculata (cowpea)  
 C>Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 20-Jun-2000  
 C:Accession: T11579  
 R:Iuchi, S.; Yamaguchi-Shinozaki, K.; Urao, T.; Shinozaki, K.  
 J. Plant Res. 109, 415-424, 1996  
 A>Title: Characterization of two cDNAs for novel drought-inducible genes in the highly d  
 A:Reference number: Z17293  
 A:Accession: T11579  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-267 <IUC>  
 A:Cross-references: EMBL:D88121  
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 4.8%; Score 13; DB 2; Length 267;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 177 AVELGQFGRVNC 189  
 Db 178 AVELGQFGRVNC 190  
 RESULT 5  
 S39737  
 glucose 1-dehydrogenase homolog ywfd - Bacillus subtilis  
 N:Alternate names: protein ipa-82d  
 N:Contains: probable dehydrogenase (EC 1.1.1.-)  
 C:Species: Bacillus subtilis  
 C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000  
 C:Accession: S39737; E70035  
 R:Glaser, P.; Kunst, F.; Arnaud, M.; Coudart, M.P.; Gonzales, W.; Hullo, M.F.; Ionescu,



A.; Rapoport, G.; Danchin, A.  
Mol. Microbiol. 10, 371-384, 1993  
A:Title: Bacillus subtilis genome project: cloning and sequencing of the 97 kb region fr  
A:Reference number: S39655; MUID:95020537; PMID:7934828  
A:Accession: S39737  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-255 <GLA>  
A:Cross-references: EMBL:X73124; NID:9413923; PIDN:CAA51638.1; PID:g414006  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1993  
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte  
C.; Ehrlich, S.; Brouillet, S.; Prtchi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch  
A.; Brnlich, S.D.; Emmeron, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen  
tech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.P.  
Koetter, P.; Koningstein, G.; Krog, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,  
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seror  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yanane, K.; Yasumoto, K.; Yata, K.; Yoshida, K  
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A:Reference number: A69580; MUID:98044033; PMID:9384377  
A:Accession: E70055  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-255 <KUN>  
A:Cross-references: GB:299123; GB:AL009126; NID:g2636240; PIDN:CAB15799.1; PID:g2636308  
A:Experimental source: strain 168  
C:Genetics:  
A:Gene: wvfd  
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology  
C:Keywords: NAD; oxidoreductase  
F:8-185/Domain: short-chain alcohol dehydrogenase homology <SADH>  
  
Query Match 3.7%; Score 10; DB 1; Length 255;  
Best Local Similarity 100.0%; Pred. No. 0.039;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 17 LITGASGIG 26  
Db 11 LITGASGIG 20  
|||||  
|  
  
RESULT 6  
C87434  
2-deoxy-D-gluconate 3-dehydrogenase [imported] - Caulobacter crescentus  
C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001  
C:Accession: C87434  
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapito, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A:Title: Complete Genome Sequence of Caulobacter crescentus.  
A:Reference number: A87249; MUID:21173698; PMID:11259647  
A:Accession: C87434  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-255 <STO>  
A:Cross-references: GB:AE005673; NID:gl3422867; PIDN:AAK23471.1; GSPDB:GN00148  
C:Genetics:  
A:Gene: CCI492  
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology  
  
Query Match 3.7%; Score 10; DB 2; Length 255;  
Best Local Similarity 100.0%; Pred. No. 0.039;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 11 LEGKVALITG 20  
Db 11 LEGKVALITG 20  
|||||  
|  
  
RESULT 9  
F96563  
hypothetical protein F19K6.3 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001  
C:Accession: F96563  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar, K.;

Db 7 LEGKVALITG 16  
|||||  
|  
  
RESULT 7  
AD2307  
hypothetical protein alr4011 [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp. PCC 7120  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
C:Accession: AD2307  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yanada, M.; Yasuda, M.; Tabata, S  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AD2307  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-256 <KUR>  
A:Cross-references: GB:BA000019; PIDN:BAB75710.1; PID:g17133146; GSPDB:GN00179  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: alr4011  
  
Query Match 3.7%; Score 10; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.039;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 17 LITGASGIG 26  
Db 24 LITGASGIG 33  
|||||  
|  
  
RESULT 8  
AB3545  
toluenesulfonate zinc-independent alcohol dehydrogenase [imported] - Brucella melitensis  
C:Species: Brucella melitensis  
C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 15-Feb-2002  
C:Accession: AB3545  
R:DeIvecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,  
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess  
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis  
A:Reference number: AD3252; PMID:11756688  
A:Accession: AB3545  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-262 <KUR>  
A:Cross-references: GB:AE008918; PIDN:AAL53525.1; PID:g17984431; GSPDB:GN00191  
A:Experimental source: strain 16M  
C:Genetics:  
A:Gene: BMEII0283  
A:Map position: 11  
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology  
  
Query Match 3.7%; Score 10; DB 2; Length 262;  
Best Local Similarity 100.0%; Pred. No. 0.04;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 11 LEGKVALITG 20  
Db 13 LEGKVALITG 22  
|||||  
|  
  
RESULT 9  
F96563  
hypothetical protein F19K6.3 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001  
C:Accession: F96563  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar, K.;

ansen, N.R.; Hughes, B.; Huizar, L.  
 Nature 406, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.  
 A:Reference number: A86141; MUID:21016719; PMID:11130712  
 A:Accession: F96563  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-285 <STO>  
 A:CROSS-references: GB:AE005173; NID:gi0645436; PIDN:AA021552.1; GSPDB:GN00141  
 C:Genetics:  
 A:Gene: F19K6.3  
 A:Map position: 1  
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.7%; Score 10; DB 2; Length 285;  
 Best Local Similarity 100.0%; Pred. No. 0.043;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 KVALITGGA 22  
 Db 20 KVALITGGA 29

RESULT 10  
 PC4213  
 bphB protein - Comamonas testosteroni (fragment)  
 C:Species: Comamonas testosteroni  
 C:Date: 17-Dec-1996 #sequence\_revision 21-Jan-1997 #text\_change 08-Oct-1999  
 C:Accession: PC4213  
 R:Syvestre, M.; Sirois, M.; Hurtubise, Y.; Bergeron, J.; Ahmad, D.; Shareck, F.; Barria  
 Gene 174, 195-202, 1996  
 A:Title: Sequencing of Comamonas testosteroni strain B-356-biphenyl/chlorobiphenyl dioxy  
 A:Reference number: JC4993; MUID:97045812; PMID:8890734  
 A:Accession: PC4213  
 A:Molecule type: DNA  
 A:Residues: 1-15 <SVL>  
 A:CROSS-references: GB:U47637; NID:q1245151; PIDN:AAC44530.1; PID:q1245156  
 A:Experimental source: strain B-356  
 C:Genetics:  
 A:Gene: bphB

Query Match 3.3%; Score 9; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.034;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 VALITGGAS 23  
 Db 7 VALITGGAS 15

RESULT 11  
 B82680  
 pteridine reductase 1 xpl1457 [imported] - Xylella fastidiosa (strain 9a5c)  
 C:Species: Xylella fastidiosa  
 C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Sep-2000  
 C:Accession: B82680  
 R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen  
 Nature 406, 151-157, 2000  
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
 A:Reference number: A83515; MUID:20365717; PMID:10910347  
 A:Note: for a complete list of authors see reference number A59328 below  
 A:Accession: B82680  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-245 <SIM>  
 A:CROSS-references: GB:AE003975; GB:AE003849; NID:99106468; PIDN:AAF84266.1; GSPDB:GN001  
 A:Experimental source: strain 9a5c  
 A:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H.  
 as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.  
 submitted to GenBank, June 2000  
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohne  
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre  
 chado, M.A.; Madair, A.M.B.N.; Madsen, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.  
 A:Authors: Martins, E.M.F.; Matsukuma, A.I.; Menck, C.F.M.; Miracca, R.C.; Miyaki, C.Y.;  
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.  
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak  
 A:Authors: da Silva, A.C.R.; da Silva, P.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira  
 M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za  
 A:Reference number: A59328  
 A:Contents: annotation  
 A:Molecule type: DNA  
 A:Residues: 1-257 <STO>  
 A:CROSS-references: GB:AE002093; NID:93522935; PIDN:AAC34217.1; GSPDB:GN00139  
 C:Genetics:  
 A:Gene: At2g47130; F14M4.4  
 A:Map position: 2  
 A:Introns: 5/2  
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.3%; Score 9; DB 2; Length 257;  
 Best Local Similarity 100.0%; Pred. No. 0.42;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ITGGASGIG 26  
 Db 13 ITGGASGIG 21

RESULT 13  
 T02176  
 probable alcohol dehydrogenase At2g47120 [imported] - Arabidopsis thaliana  
 A:Alternate names: hypothetical protein F14M4.5

Query Match 3.3%; Score 9; DB 2; Length 245;  
 Best Local Similarity 100.0%; Pred. No. 0.41;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 KVALITGGA 22  
 Db 6 KVALITGGA 14

RESULT 12  
 T02175  
 probable alcohol dehydrogenase At2g47130 [imported] - Arabidopsis thaliana  
 A:Alternate names: hypothetical protein F14M4.4  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 16-Feb-2001  
 C:Accession: T02175; D84911  
 R:Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, M.; Rom  
 submitted to the EMBL Data Library, September 1998  
 A:Description: Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence.  
 A:Reference number: Z14609  
 A:Accession: T02175  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-257 <ROU>  
 A:CROSS-references: EMBL:AC004411; NID:93522932; PID:93522935  
 A:Experimental source: cultivar Columbia  
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon, L.  
 ess, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J  
 Nature 402, 761-768, 1999  
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A:Reference number: A84420; MUID:20083487; PMID:10617197  
 A:Accession: D84911  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-257 <STO>  
 A:CROSS-references: GB:AE002093; NID:93522935; PIDN:AAC34217.1; GSPDB:GN00139  
 C:Genetics:  
 A:Gene: At2g47130; F14M4.4  
 A:Map position: 2  
 A:Introns: 5/2  
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.3%; Score 9; DB 2; Length 257;  
 Best Local Similarity 100.0%; Pred. No. 0.42;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ITGGASGIG 26  
 Db 13 ITGGASGIG 21

RESULT 13  
 T02176  
 probable alcohol dehydrogenase At2g47120 [imported] - Arabidopsis thaliana  
 A:Alternate names: hypothetical protein F14M4.5

C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 16-Feb-2001  
C;Accession: T02176; C84911  
R;Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, M.; Rounsley, S.D.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
submitted to the EMBL Data Library, September 1998  
A;Description: Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence.  
A;Reference number: Z14609  
A;Accession: T02176  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-258 <ROU>  
A;Cross-references: EMBL:AC004411; NID:G3522932; PID:G3522936  
A;Experimental source: cultivar Columbia  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A;Reference number: A84420; MUID:20083487; PMID:10617197  
A;Accession: C84911  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-258 <STO>  
A;Cross-references: GB:AE002093; NID:G3522936; PIDN:AAC34218.1; GSPDB:GN00139  
C;Genetics:  
A;Gene: At2g47120; F14M4.5  
A;Map position: 2  
A;Introns: 5/2  
A;Note: F14M4.5  
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.3%; Score 9; DB 2; Length 258;  
Best Local Similarity 100.0%; Pred. No. 0.42;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ITGASGIG 26  
|||||  
Db 13 ITGASGIG 21

## RESULT 14

H75616  
oxidoreductase, short-chain dehydrogenase/reductase family - Deinococcus radiodurans (st  
C;Species: Deinococcus radiodurans  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000  
C;Accession: H75616  
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
S.; Smith, H.O.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma  
Science 286, 1571-1577, 1999  
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A;Reference number: A75250; MUID:20036896; PMID:10567266  
A;Accession: H75616  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-258 <WHI>  
A;Cross-references: GB:AB001862; GB:AE001825; NID:G6460468; PIDN:AAF12180.1; PID:G646047  
A;Experimental source: strain R1  
C;Genetics:  
A;Gene: DRA0200  
A;Map position: 2  
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.3%; Score 9; DB 2; Length 258;  
Best Local Similarity 100.0%; Pred. No. 0.42;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 GKVALITGG 21  
|||||  
Db 11 GKVALITGG 19

## RESULT 15

AI3149  
3-oxoacyl-(acyl-carrier protein) reductase [imported] - Agrobacterium tumefaciens (strai  
C;Species: Agrobacterium tumefaciens  
C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002  
C;Accession: AI3149  
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell  
; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Kreepan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.  
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A;Reference number: AB2577; MUID:21608550; PMID:11743193  
A;Accession: AI3149  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-259 <KUR>  
A;Cross-references: GB:AE008689; PIDN:AAL45615.1; PID:gl7743336; GSPDB:GN00187  
A;Experimental source: strain C58 (Dupont)  
C;Genetics:  
A;Gene: fabG  
A;Map position: linear chromosome  
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 3.3%; Score 9; DB 2; Length 259;  
Best Local Similarity 100.0%; Pred. No. 0.43;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ITGASGIG 26  
|||||  
Db 14 ITGASGIG 22

Search completed: October 23, 2003, 13:05:55  
Job time : 85 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 23, 2003, 12:52:05 ; Search time 23 Seconds  
(without alignments)  
558.187 Million cell updates/sec

Title: US-09-673-918A-2

Perfect score: 273

Sequence: 1 MQLRTAPARRLEKVALITG.....IDGGSVCNSVIKVFQVPS 273

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	4.4	250	1 LINX_PSEPA	P50198 pseudomonas
2	10	3.7	255	1 YWFD_BACSU	P39640 bacillus su
3	10	3.7	261	1 BPHB_BOVIN	O02691 bos taurus
4	10	3.7	281	1 BPHB_COMTE	O46381 c cis-2,3-d
5	9	3.3	285	1 GS19_BACSU	P80873 bacillus su
6	9	3.3	689	1 YUXG_BACSU	P40747 bacillus su
7	8	2.9	253	1 KDUD_ERWCH	Q05528 erwinia chr
8	8	2.9	267	1 SORD_KLEPN	P37079 klebsiella
9	8	2.9	275	1 BPHB_PSEPS	P08694 p cis-2,3-d
10	8	2.9	277	1 BPHB_BURCE	P47227 b cis-2,3-d
11	8	2.9	277	1 BPHB_PSRPU	P72220 p cis-2,3-d
12	8	2.9	449	1 GSHR_BURCE	P48639 burkholderi
13	7	2.6	136	1 R27A_SCHPO	O14388 schizosacch
14	7	2.6	153	1 GLB2_ASCSU	P49672 ascaris suu
15	7	2.6	154	1 YOSB_CABEL	Q09254 caenorhabdi
16	7	2.6	167	1 PSAG_SPIOL	P12357 spinacia ol
17	7	2.6	214	1 Y540_AQUAE	O66819 aquifex aeo
18	7	2.6	244	1 FABG_VIBCH	Q06819 vibrio chol
19	7	2.6	255	1 YN32_YEAST	Q03798 saccharomyc
20	7	2.6	260	1 HCD2_RAT	O70351 rattus norv
21	7	2.6	261	1 HCD2_HUMAN	Q09714 homo sapien
22	7	2.6	275	1 DAPF_SHEON	O89h5 shewanella
23	7	2.6	282	1 T4HR_MAGGR	Q12634 magnaporthe
24	7	2.6	295	1 SP19_YEAST	P32573 saccharomyc
25	7	2.6	305	1 LIGD_PSEPA	Q01198 pseudomonas
26	7	2.6	340	1 APEB_EUCAP	O85292 buchnera ap
27	7	2.6	368	1 GMD1_CABEL	Q18801 caenorhabdi
28	7	2.6	373	1 GMD1_ECOLI	P32054 escherichia
29	7	2.6	373	1 GMD1_VIBCH	Q06952 vibrio chol
30	7	2.6	378	1 YK84_CABEL	P34350 caenorhabdi
31	7	2.6	382	1 GMD2_CABEL	O45583 caenorhabdi
32	7	2.6	387	1 GMD5_DROME	Q9vmw9 drosophila
33	7	2.6	397	1 RL3_DICDI	P34113 dictyosteli

34	7	2.6	414	1 YOAB_BACSU	O34864 bacillus su
35	7	2.6	459	1 GSHR_ANASP	P48638 anabaena sp
36	7	2.6	569	1 ATKB_SALT1	Q2865 salmonella
37	7	2.6	648	1 AMO1_ARTS1	Q07121 arthrobacte
38	7	2.6	648	1 AMO2_ARTS1	Q07123 arthrobacte
39	7	2.6	682	1 ATKB_SALT1	Q82q2 salmonella
40	7	2.6	737	1 KNS1_YEAST	P32350 saccharomyc
41	7	2.6	796	1 DHG_ECOLI	P15877 escherichia
42	7	2.6	824	1 VPP3_HUMAN	Q13099 homo sapien
43	7	2.6	830	1 VPP3_HUMAN	Q13488 h vacuolar
44	7	2.6	858	1 PDG1_ARATH	Q5053 arabidopsis
45	7	2.6	923	1 ODOI_BUCAP	Q8k9n3 buchnera ap
46	7	2.6	934	1 ODOI_COXBU	P51056 coxiella bu
47	7	2.6	942	1 ZDS2_YEAST	P54786 saccharomyc
48	7	2.6	1036	1 Y946_ARCFU	O29316 archaeoglob
49	7	2.6	2670	1 YAO5_SCHPO	Q10105 schizosacch
50	6	2.2	80	1 H3_HORVU	P06353 hordeum vul
51	6	2.2	83	1 HEPC_MOUSE	Q9eq21 mus musculu
52	6	2.2	85	1 Y522_PSEAE	Q51483 pseudomonas
53	6	2.2	89	1 CYB_BRANA	P49390 brassica na
54	6	2.2	89	1 FLIO_SALT1	P54701 salmonella
55	6	2.2	99	1 SR19_PYRAB	Q9v119 pyrococcus
56	6	2.2	102	1 B1_BEV	P29099 black beetl
57	6	2.2	102	1 TRPR_PASMU	Q9cnu9 pasteurella
58	6	2.2	105	1 RL21_RICPR	Q9zc19 rickettsia
59	6	2.2	115	1 Y112_METMA	Q8q0m4 methanosarc
60	6	2.2	115	1 YW69_METAC	O8tkx4 methanosarc
61	6	2.2	119	1 YF56_PYRFU	Q8u0n0 pyrococcus
62	6	2.2	126	1 ACP8_YERPE	Q8zcp5 yersinia pe
63	6	2.2	128	1 NCAP_LELV	Q04558 lelystad vi
64	6	2.2	130	1 YG31_PYRHO	O59297 pyrococcus
65	6	2.2	133	1 NL21_PARJU	P55958 parietaria
66	6	2.2	133	1 NL22_PARJU	O04043 parietaria
67	6	2.2	135	1 H32_MEDSA	P11105 medicago sa
68	6	2.2	135	1 H33_ARATH	P59169 arabidopsis
69	6	2.2	137	1 YAEU_PSEPU	P45388 pseudomonas
70	6	2.2	137	1 YB47_SYNY3	P73795 synechocyst
71	6	2.2	140	1 HBA1_TRAST	P04237 tragelaphus
72	6	2.2	141	1 HBA1_BOSMU	P01967 bos mutus g
73	6	2.2	141	1 HBA1_BUBBU	Q9tsn7 bubalus bub
74	6	2.2	141	1 HBA1_BOSMU	P01968 bos mutus g
75	6	2.2	141	1 HBA2_BUBBU	Q9tsn8 bubalus bub
76	6	2.2	141	1 HBA3_BUBBU	Q9tsn9 bubalus bub
77	6	2.2	141	1 HBA4_BUBBU	Q9xsk1 bubalus bub
78	6	2.2	141	1 HBA1_BISBO	P09423 bison bonas
79	6	2.2	141	1 HBA_BOSCP	P01969 bos gaurus
80	6	2.2	141	1 HBA_BOVIN	P01966 bos taurus
81	6	2.2	143	1 RS23_SCHPO	P79057 schizosacch
82	6	2.2	145	1 RS23_NEUCR	Q9he74 neurospora
83	6	2.2	145	1 RS23_YEAST	P32827 saccharomyc
84	6	2.2	150	1 YL20_ARCFU	O28160 archaeoglob
85	6	2.2	158	1 FCY1_YEAST	Q12178 saccharomyc
86	6	2.2	159	1 GREB_BUCAI	P57464 buchnera ap
87	6	2.2	163	1 SAK_BPP42	P15240 bacterioph
88	6	2.2	163	1 SAK_STAAM	P00802 staphylococ
89	6	2.2	172	1 Y941_TREPA	O83911 treponema p
90	6	2.2	174	1 LEU2_RHET	Q8vma6 rhizobium e
91	6	2.2	174	1 MAUL_MEIME	Q50234 methylophil
92	6	2.2	174	1 RS5_SYNEL	P59126 synechococc
93	6	2.2	175	1 KDGL_SYNY3	Q55143 synechocyst
94	6	2.2	177	1 NRFL_WOLSU	Q98166 wolinnella s
95	6	2.2	180	1 YRBI_HABIN	P45314 haemophilus
96	6	2.2	187	1 AHPC_BACSU	P450239 bacillus su
97	6	2.2	193	1 SYFB_ERWCH	P37984 erwinia chr
98	6	2.2	194	1 COAE_AGRTS	Q8u4c4 agrobacteri
99	6	2.2	197	1 Y0G8_YERPE	P58636 yersinia pe
100	6	2.2	200	1 RRNB_SCHPO	O94332 schizosacch
101	6	2.2	201	1 FABG_BRANA	P27582 brassica na
102	6	2.2	209	1 RNFG_YERPE	Q8zed3 yersinia pe
103	6	2.2	210	1 ALKF_TREPA	O83578 t putative
104	6	2.2	211	1 KAD_TREPA	O83604 treponema p
105	6	2.2	211	1 YBS1_YEAST	P38243 saccharomyc
106	6	2.2	213	1 PA3L_MOUSE	Q9c6b4 mus musculu

107	1	214	6	2.2	6	2.2	180	1	282	6	2.2	282	1	ARDH_YEAST	P50166	candida tro
108	1	216	6	2.2	6	2.2	181	1	283	6	2.2	283	1	AP10_YEAST	P3068	saccharomyc
109	1	217	6	2.2	6	2.2	182	1	285	6	2.2	285	1	YHXC_BACSU	P40397	bacillus su
110	1	218	6	2.2	6	2.2	183	1	292	6	2.2	292	1	EFTS_XANCP	Q8pav3	xanthomonas
111	1	219	6	2.2	6	2.2	184	1	292	6	2.2	292	1	EFTS_XANCP	Q8pav3	xanthomonas
112	1	220	6	2.2	6	2.2	185	1	297	6	2.2	297	1	OXIR_STRLI	P53120	streptomyce
113	1	221	6	2.2	6	2.2	186	1	298	6	2.2	298	1	OXIR_STRLI	Q03326	streptomyce
114	1	222	6	2.2	6	2.2	187	1	300	6	2.2	300	1	ERA_MYCTU	O05834	mycobacteri
115	1	223	6	2.2	6	2.2	188	1	301	6	2.2	301	1	YJHH_ECOLI	P93359	escherichia
116	1	224	6	2.2	6	2.2	189	1	310	6	2.2	310	1	YJHH_ECOLI	P93359	escherichia
117	1	225	6	2.2	6	2.2	190	1	311	6	2.2	311	1	YJHH_ECOLI	P93359	escherichia
118	1	226	6	2.2	6	2.2	191	1	311	6	2.2	311	1	YJHH_ECOLI	P93359	escherichia
119	1	227	6	2.2	6	2.2	192	1	314	6	2.2	314	1	YJHH_ECOLI	P93359	escherichia
120	1	228	6	2.2	6	2.2	193	1	315	6	2.2	315	1	YJHH_ECOLI	P93359	escherichia
121	1	229	6	2.2	6	2.2	194	1	315	6	2.2	315	1	YJHH_ECOLI	P93359	escherichia
122	1	230	6	2.2	6	2.2	195	1	316	6	2.2	316	1	YJHH_ECOLI	P93359	escherichia
123	1	231	6	2.2	6	2.2	196	1	316	6	2.2	316	1	YJHH_ECOLI	P93359	escherichia
124	1	232	6	2.2	6	2.2	197	1	316	6	2.2	316	1	YJHH_ECOLI	P93359	escherichia
125	1	233	6	2.2	6	2.2	198	1	319	6	2.2	319	1	YJHH_ECOLI	P93359	escherichia
126	1	234	6	2.2	6	2.2	199	1	320	6	2.2	320	1	YJHH_ECOLI	P93359	escherichia
127	1	235	6	2.2	6	2.2	200	1	322	6	2.2	322	1	YJHH_ECOLI	P93359	escherichia
128	1	236	6	2.2	6	2.2	201	1	323	6	2.2	323	1	YJHH_ECOLI	P93359	escherichia
129	1	237	6	2.2	6	2.2	202	1	323	6	2.2	323	1	YJHH_ECOLI	P93359	escherichia
130	1	238	6	2.2	6	2.2	203	1	323	6	2.2	323	1	YJHH_ECOLI	P93359	escherichia
131	1	239	6	2.2	6	2.2	204	1	326	6	2.2	326	1	YJHH_ECOLI	P93359	escherichia
132	1	240	6	2.2	6	2.2	205	1	330	6	2.2	330	1	YJHH_ECOLI	P93359	escherichia
133	1	241	6	2.2	6	2.2	206	1	330	6	2.2	330	1	YJHH_ECOLI	P93359	escherichia
134	1	242	6	2.2	6	2.2	207	1	331	6	2.2	331	1	YJHH_ECOLI	P93359	escherichia
135	1	243	6	2.2	6	2.2	208	1	331	6	2.2	331	1	YJHH_ECOLI	P93359	escherichia
136	1	244	6	2.2	6	2.2	209	1	331	6	2.2	331	1	YJHH_ECOLI	P93359	escherichia
137	1	245	6	2.2	6	2.2	210	1	332	6	2.2	332	1	YJHH_ECOLI	P93359	escherichia
138	1	246	6	2.2	6	2.2	211	1	332	6	2.2	332	1	YJHH_ECOLI	P93359	escherichia
139	1	247	6	2.2	6	2.2	212	1	332	6	2.2	332	1	YJHH_ECOLI	P93359	escherichia
140	1	248	6	2.2	6	2.2	213	1	335	6	2.2	335	1	YJHH_ECOLI	P93359	escherichia
141	1	249	6	2.2	6	2.2	214	1	336	6	2.2	336	1	YJHH_ECOLI	P93359	escherichia
142	1	250	6	2.2	6	2.2	215	1	336	6	2.2	336	1	YJHH_ECOLI	P93359	escherichia
143	1	251	6	2.2	6	2.2	216	1	337	6	2.2	337	1	YJHH_ECOLI	P93359	escherichia
144	1	252	6	2.2	6	2.2	217	1	338	6	2.2	338	1	YJHH_ECOLI	P93359	escherichia
145	1	253	6	2.2	6	2.2	218	1	338	6	2.2	338	1	YJHH_ECOLI	P93359	escherichia
146	1	254	6	2.2	6	2.2	219	1	339	6	2.2	339	1	YJHH_ECOLI	P93359	escherichia
147	1	255	6	2.2	6	2.2	220	1	339	6	2.2	339	1	YJHH_ECOLI	P93359	escherichia
148	1	256	6	2.2	6	2.2	221	1	343	6	2.2	343	1	YJHH_ECOLI	P93359	escherichia
149	1	257	6	2.2	6	2.2	222	1	344	6	2.2	344	1	YJHH_ECOLI	P93359	escherichia
150	1	258	6	2.2	6	2.2	223	1	345	6	2.2	345	1	YJHH_ECOLI	P93359	escherichia
151	1	259	6	2.2	6	2.2	224	1	345	6	2.2	345	1	YJHH_ECOLI	P93359	escherichia
152	1	260	6	2.2	6	2.2	225	1	346	6	2.2	346	1	YJHH_ECOLI	P93359	escherichia
153	1	261	6	2.2	6	2.2	226	1	347	6	2.2	347	1	YJHH_ECOLI	P93359	escherichia
154	1	262	6	2.2	6	2.2	227	1	347	6	2.2	347	1	YJHH_ECOLI	P93359	escherichia
155	1	263	6	2.2	6	2.2	228	1	347	6	2.2	347	1	YJHH_ECOLI	P93359	escherichia
156	1	264	6	2.2	6	2.2	229	1	347	6	2.2	347	1	YJHH_ECOLI	P93359	escherichia
157	1	265	6	2.2	6	2.2	230	1	347	6	2.2	347	1	YJHH_ECOLI	P93359	escherichia
158	1	266	6	2.2	6	2.2	231	1	347	6	2.2	347	1	YJHH_ECOLI	P93359	escherichia
159	1	267	6	2.2	6	2.2	232	1	347	6	2.2	347	1	YJHH_ECOLI	P93359	escherichia
160	1	268	6	2.2	6	2.2	233	1	347	6	2.2	347	1	YJHH_ECOLI	P93359	escherichia
161	1	269	6	2.2	6	2.2	234	1	348	6	2.2	348	1	YJHH_ECOLI	P93359	escherichia
162	1	270	6	2.2	6	2.2	235	1	348	6	2.2	348	1	YJHH_ECOLI	P93359	escherichia
163	1	271	6	2.2	6	2.2	236	1	348	6	2.2	348	1	YJHH_ECOLI	P93359	escherichia
164	1	272	6	2.2	6	2.2	237	1	353	6	2.2	353	1	YJHH_ECOLI	P93359	escherichia
165	1	273	6	2.2	6	2.2	238	1	353	6	2.2	353	1	YJHH_ECOLI	P93359	escherichia
166	1	274	6	2.2	6	2.2	239	1	353	6	2.2	353	1	YJHH_ECOLI	P93359	escherichia
167	1	275	6	2.2	6	2.2	240	1	354	6	2.2	354	1	YJHH_ECOLI	P93359	escherichia
168	1	276	6	2.2	6	2.2	241	1	354	6	2.2	354	1	YJHH_ECOLI	P93359	escherichia
169	1	277	6	2.2	6	2.2	242	1	354	6	2.2	354	1	YJHH_ECOLI	P93359	escherichia
170	1	278	6	2.2	6	2.2	243	1	355	6	2.2	355	1	YJHH_ECOLI	P93359	escherichia
171	1	279	6	2.2	6	2.2	244	1	355	6	2.2	355	1	YJHH_ECOLI	P93359	escherichia
172	1	280	6	2.2	6	2.2	245	1	357	6	2.2	357	1	YJHH_ECOLI	P93359	escherichia
173	1	281	6	2.2	6	2.2	246	1	357	6	2.2	357	1	YJHH_ECOLI	P93359	escherichia
174	1	282	6	2.2	6	2.2	247	1	359	6	2.2	359	1	YJHH_ECOLI	P93359	escherichia
175	1	283	6	2.2	6	2.2	248	1	359	6	2.2	359	1	YJHH_ECOLI	P93359	escherichia
176	1	284	6	2.2	6	2.2	249	1	361	6	2.2	361	1	YJHH_ECOLI	P93359	escherichia
177	1	285	6	2.2	6	2.2	250	1	363	6	2.2	363	1	YJHH_ECOLI	P93359	escherichia
178	1	286	6	2.2	6	2.2	251	1	363	6	2.2	363	1	YJHH_ECOLI	P93359	escherichia
179	1	287	6	2.2	6	2.2	252	1	365	6	2.2	365	1	YJHH_ECOLI	P93359	escherichia

253	1	366	1	APN1_SCHPO	P50525 schizosacch	326	6	2.2	457	1	ARLY_PASMU	P57909 pasteurella
254	1	366	1	HEMA_INBID	P12441 influenza b	327	6	2.2	457	1	DNAA_UREPA	Q9pre2 ureaplasma
255	1	366	1	NOLL_RHISN	P55431 rhizobium s	328	6	2.2	457	1	PROV_ECOLI	P7327 escherichia
256	1	367	1	MX12_HUMAN	P53778 homo sapien	329	6	2.2	458	1	SSU1_YEAST	P41930 saccharomyc
257	1	367	1	MPAL_JUNAS	P81294 juniperus a	330	6	2.2	460	1	NU4M_CROLA	P34194 crossostoma
258	1	368	1	PRD2_STRCO	Q9kxr7 streptomyce	331	6	2.2	461	1	NU4M_YEAST	P32363 saccharomyc
259	1	368	1	REF2_STRCO	Q53915 streptomyce	332	6	2.2	461	1	Y514_HUMAN	O60269 homo sapien
260	1	369	1	CHEB_RHOSH	O33558 rhodobacter	333	6	2.2	463	1	COAT_FRG3V	Q67473 frog virus
261	1	370	1	HEM2_CORGL	Q8nqal corynebacte	334	6	2.2	463	1	COAT_RTRV	Q91qz8 rana tigrin
262	1	371	1	H2AW_HUMAN	O9p0m6 homo sapien	335	6	2.2	463	1	SIL9_HUMAN	Q9y336 homo sapien
263	1	372	1	GND5_HUMAN	O60547 homo sapien	336	6	2.2	463	1	YGL1_YEAST	P53136 saccharomyc
264	1	374	1	SBP_CRIYA	P18632 cryptospori	337	6	2.2	464	1	CAPB_BACAN	P19580 bacillus an
265	1	376	1	ACT_CRYPV	P26183 cryptospori	338	6	2.2	464	1	GSHR_SCHPO	P78965 schizosacch
266	1	377	1	PRD2_COREF	Q8ftc6 corynebacte	339	6	2.2	465	1	CRU4_BRANA	P33522 brassica na
267	1	377	1	RIM2_YEAST	P38127 saccharomyc	340	6	2.2	465	1	MPPB_BLAEM	Q00302 blastoclad
268	1	378	1	YN91_ANASP	P46080 anabaena sp	341	6	2.2	467	1	SIL7_HUMAN	Q9y286 homo sapien
269	1	379	1	VAT1_TORCA	P19333 torpedo cal	342	6	2.2	468	1	DCMG_METTE	Q50539 methanosarc
270	1	380	1	COTB_BACSU	P07789 bacillus su	343	6	2.2	468	1	YB07_HAEIN	Q57007 haemophilus
271	1	380	1	MEDH_BACWT	P31005 bacillus me	344	6	2.2	469	1	LEU2_AGRIS	Q8ubv9 agrobacteri
272	1	380	1	YCX7_ODOSI	P49833 odontella s	345	6	2.2	469	1	LEU2_RHIL0	Q98efi rhizobium l
273	1	384	1	RECF_SYNY3	P73532 synechocyst	346	6	2.2	469	1	LEU2_RHIME	Q92176 rhizobium m
274	1	385	1	DIAC_HUMAN	Q01459 homo sapien	347	6	2.2	470	1	SELA_MOOTH	Q33277 morella th
275	1	385	1	VATC_MANSE	Q9u5n1 manduca sex	348	6	2.2	472	1	PEDA_STRPY	Q9a0m0 streptococc
276	1	386	1	HIS2_RALUSO	Q9y020 ralstonia s	349	6	2.2	473	1	T115_CLOPE	Q05309 clostridium
277	1	386	1	XYLA_STROL	P15587 streptomyce	350	6	2.2	474	1	DLDH_ALCEU	P52992 alcaligenes
278	1	387	1	S17P_SPTOL	O20252 spinacia ol	351	6	2.2	476	1	CBPH_HUMAN	P16870 homo sapien
279	1	387	1	T2C_PARTE	Q27181 paramacium	352	6	2.2	476	1	CBPH_MOUSE	Q00493 mus musculu
280	1	387	1	XYLA_STRCO	Q10b8 streptomyce	353	6	2.2	476	1	CBPH_RAT	P15087 rattus norv
281	1	387	1	XYLA_STRRU	P24300 streptomyce	354	6	2.2	477	1	DLDH_PSEFL	P14218 pseudomonas
282	1	388	1	CYB_MAIZE	P04165 zea mays (m	355	6	2.2	477	1	TRPC_HAEIN	P46451 haemophilus
283	1	388	1	XYLA_STRDI	P50910 streptomyce	356	6	2.2	479	1	6PGD_TRYBB	P31072 trypanosoma
284	1	388	1	XYLA_STRTM	Q91558 streptomyce	357	6	2.2	481	1	LMRA_STRLN	P46104 streptomyce
285	1	390	1	XYLA_STRAL	P24299 streptomyce	358	6	2.2	483	1	KPYK_METEX	O05118 methylobact
286	1	392	1	CYB_BEA	Q9z2t8 pisum sativ	359	6	2.2	484	1	PANF_HAEIN	P44963 haemophilus
287	1	392	1	CYB_SOLTU	P29757 solanum tub	360	6	2.2	485	1	SAHH_PETCR	Q01781 petrobelinu
288	1	392	1	CYB_VICFA	P05718 vicia faba	361	6	2.2	487	1	YOW5_CABEL	P30651 caenorhabdi
289	1	393	1	CYB_ARATH	P42792 arabidopsis	362	6	2.2	488	1	GATA_AERPE	Q9yb80 aeropyrum p
290	1	393	1	NIFS_BRAJA	P37030 bradyrhizob	363	6	2.2	492	1	YD48_SCHPO	Q10301 schizosacch
291	1	394	1	CYB_DENBE	P09843 oenothera b	364	6	2.2	496	1	GSHR_ORYSA	P48642 oryza sativ
292	1	396	1	YC44_CYACA	O19913 cyanidium c	365	6	2.2	497	1	DHAL_ENCBU	Q27640 enchytraeus
293	1	397	1	CYB_ORYSA	P14833 oryza sativ	366	6	2.2	497	1	FXD2_HUMAN	O60548 homo sapien
294	1	398	1	CYB_DAUCA	Q94s37 daucus caro	367	6	2.2	498	1	FLID_BACSU	P39738 bacillus su
295	1	398	1	CYB_WHEAT	P07747 triticum ae	368	6	2.2	499	1	ABFB_ASPNG	P42255 aspergillus
296	1	402	1	RNBP_PIG	P17560 sus scrofa	369	6	2.2	500	1	IC1_HUMAN	P05155 homo sapien
297	1	404	1	KIME_SCHPO	Q09780 schizosacch	370	6	2.2	501	1	CKX2_ARATH	Q9fuj3 arabidopsis
298	1	405	1	THRC_METJA	Q58860 methanococc	371	6	2.2	502	1	MYOC_RAT	Q9rlj4 rattus norv
299	1	406	1	CSDB_ECOLI	P77444 escherichia	372	6	2.2	509	1	AURE_STAAU	P81177 staphylococ
300	1	407	1	SYI_MYCGE	P47693 mycoplasma	373	6	2.2	510	1	ERM_HUMAN	P41161 homo sapien
301	1	413	1	NEUA_STR3A	Q53598 streptococc	374	6	2.2	512	1	K2C5_XENLA	P16878 xenopus lae
302	1	413	1	NEUA_STR3A	Q9afg9 streptococc	375	6	2.2	514	1	SAD1_SCHPO	O9825 schizosacch
303	1	414	1	PYRC_STR3A	Q9ahm0 thermoplas	376	6	2.2	516	1	YC82_EUGGR	P30397 euglena gra
304	1	416	1	HAPC_PIG	P17630 sus scrofa	377	6	2.2	517	1	DHA5_HUMAN	P30837 homo sapien
305	1	417	1	RNBP_HUMAN	P51606 homo sapien	378	6	2.2	520	1	AMPA_MYCSA	P47707 mycoplasma
306	1	419	1	MANA_PSEFL	P49424 pseudomonas	379	6	2.2	521	1	VL2_HPV04	Q07862 human papil
307	1	419	1	NEUA_ECOLI	P13266 escherichia	380	6	2.2	523	1	CKX3_ARATH	Q9lt83 arabidopsis
308	1	419	1	RNBP_MOUSE	P82343 mus musculu	381	6	2.2	524	1	CKX4_ARATH	Q9fui2 arabidopsis
309	1	419	1	RNBP_RAT	P51607 rattus norv	382	6	2.2	524	1	FLID_BACHD	O9k6m0 bacillus ha
310	1	425	1	SYS_DEIRA	Q9ruv5 deinococcus	383	6	2.2	532	1	MLO_HORVU	P33766 hordeum vul
311	1	431	1	TRB2_SULTO	Q970n1 sulfolobus	384	6	2.2	533	1	AMT1_CABEL	P54145 caenorhabdi
312	1	433	1	TCO1_HUMAN	P20061 homo sapien	385	6	2.2	534	1	CKX1_MAIZE	P54145 zea mays (m
313	1	438	1	MNT2_PSEAE	Q9rpf2 pseudomonas	386	6	2.2	535	1	ARS_PSEAE	P51691 pseudomonas
314	1	438	1	XYLA_RUMFL	Q9s306 ruminococcu	387	6	2.2	541	1	AAAT_RABIT	O19105 oryctolagus
315	1	439	1	RNR_THIFE	P54084 thiobacilli	388	6	2.2	541	1	ACEA_YARLI	P41555 yarrowia li
316	1	441	1	YD40_HAEIN	P44165 haemophilus	389	6	2.2	541	1	MLES_OENOE	Q48796 oenococcus
317	1	442	1	VATC_DROME	Q9v7n5 drosophila	390	6	2.2	543	1	DAL5_YEAST	P15365 saccharomyc
318	1	444	1	OPSP_PETMA	O42490 petromyzon	391	6	2.2	544	1	YC9D_SCHPO	Q09887 schizosacch
319	1	445	1	XYLA_BACNE	O08325 bacillus me	392	6	2.2	546	1	PHR2_CANAL	O13318 candida alb
320	1	445	1	V148_MYCPN	P75584 mycoplasma	393	6	2.2	546	1	PYRG_VIBPA	Q87lp9 vibrio para
321	1	447	1	GNT2_HUMAN	Q10469 h alpha-1,6	394	6	2.2	547	1	ILVD_ARCFU	O29248 archaeoglob
322	1	453	1	YEGQ_ECOLI	P76403 escherichia	395	6	2.2	548	1	PPAC_THEMEA	Q9wz56 thermotoga
323	1	454	1	YB62_HAEIN	P45217 haemophilus	396	6	2.2	552	1	K2C6_MOUSE	P50446 mus musculu
324	1	455	1	12S2_ARATH	P15456 arabidopsis	397	6	2.2	555	1	ILVD_AQUAE	Q67009 aquifex aeo
325	1	456	1	PROV_SALTY	P37460 salmonella	398	6	2.2	555	1	ILVD_BACHD	Q9k8e4 bacillus ha

999	6	2.2	556	1	RSL_HELPY	P56008 helicobacte	472	6	2.2	725	1	RNR_MYCE	P47350 mycoplasma
1000	6	2.2	556	1	SYDC_YEAST	P04802 saccharomyc	473	6	2.2	726	1	RNR_MYCPN	P75529 mycoplasma
1001	6	2.2	557	1	CAB1_AQUAE	O67869 aquifex aeo	474	6	2.2	728	1	GSHI_NEURC	Q8X0x0 neosporea
1002	6	2.2	557	1	ILVD_AERPE	Q9Y988 aeropyrum p	475	6	2.2	730	1	DCOR_LACS3	P43099 lactobacill
1003	6	2.2	557	1	ILVD_BACSU	P51785 bacillus su	476	6	2.2	730	1	FOG_DROME	P40795 drosophila
1004	6	2.2	557	1	Y369_MYCEG	P47609 mycoplasma	477	6	2.2	731	1	RNR_BUCAI	P57628 bucherna ap
1005	6	2.2	560	1	ILVD_SUITO	Q96YK0 sulfolobus	478	6	2.2	733	1	SUF_DROME	P25991 drosophila
1006	6	2.2	560	1	KGS9_YEAST	P04637 saccharomyc	479	6	2.2	736	1	PRXI_CHICK	Q91018 gallus gall
1007	6	2.2	567	1	KXSI_EMENI	P00402 emericella	480	6	2.2	737	1	PRXI_HUMAN	Q92786 homo sapien
1008	6	2.2	574	1	HEMA_INBMD	P03461 influenza b	481	6	2.2	737	1	PRXI_MOUSE	P48437 mus musculu
1009	6	2.2	575	1	HEMA_INBBO	P10448 influenza b	482	6	2.2	751	1	PA26_RAT	P79750 rattus norv
1010	6	2.2	575	1	HEMA_INBHK	P03462 influenza b	483	6	2.2	752	1	PA26_MOUSE	P79781 mus musculu
1011	6	2.2	576	1	DEAL_ANASP	Q8YTW5 anabaena sp	484	6	2.2	768	1	PURL_SINY3	P72644 synechocyst
1012	6	2.2	576	1	HEMA_INBUS	P09766 influenza b	485	6	2.2	768	1	COMP_BACSU	Q99027 bacillus su
1013	6	2.2	578	1	HEMA_INBME	P09765 influenza b	486	6	2.2	781	1	IOREB_BREDI	Q51698 brevundim
1014	6	2.2	578	1	HEMA_INBVI	P09767 influenza b	487	6	2.2	782	1	RNR_HABIN	P44907 haemophilus
1015	6	2.2	578	1	VATA_METAC	Q8TJJ1 methanosarc	488	6	2.2	797	1	AF32_HUMAN	Q9Y4V6 homo sapien
1016	6	2.2	578	1	VATA_METMA	P60186 methanosarc	489	6	2.2	803	1	SYFB_WIEGBR	Q8D3B5 wiggleswort
1017	6	2.2	579	1	SYN3_RAT	O70441 rattus norv	490	6	2.2	804	1	YNA4_CAEEL	P45895 caenorhabdi
1018	6	2.2	583	1	HEMA_INBEN	P10757 influenza b	491	6	2.2	816	1	PA26_HUMAN	O60733 homo sapien
1019	6	2.2	583	1	HEMA_INBOR	P03464 influenza b	492	6	2.2	816	1	PA26_HUMAN	O60733 homo sapien
1020	6	2.2	584	1	HEMA_INBSI	P03463 influenza b	493	6	2.2	813	1	RNR_SHIFL	P21499 escherichia
1021	6	2.2	584	1	HEMA_INBLE	P03460 influenza b	494	6	2.2	814	1	P3KI_SOYBN	P42347 glycine max
1022	6	2.2	585	1	HEMA_INBEB	P17504 influenza b	495	6	2.2	817	1	PERO_HUMAN	P75420 homo sapien
1023	6	2.2	585	1	HEMA_INBEK	P22092 influenza b	496	6	2.2	821	1	YGAB_YEAST	P46951 saccharomyc
1024	6	2.2	585	1	HEMA_INBEH	P22092 influenza b	497	6	2.2	821	1	RNR_VISECH	O9BNV1 vibrio chol
1025	6	2.2	593	1	VATA_THETH	Q56403 thermus the	498	6	2.2	824	1	TG37_MOUSE	Q61371 mus musculu
1026	6	2.2	595	1	SILL_HUMAN	Q96PQ1 homo sapien	499	6	2.2	825	1	SE5_RAT	Q63003 rattus norv
1027	6	2.2	597	1	SILL_PANTR	Q95JH0 pan troglod	500	6	2.2	827	1	CSG_HALVO	P25062 halobacteri
1028	6	2.2	605	1	BLRL_EBV	P03209 epstein-bar	501	6	2.2	835	1	RNR_VIBPA	P40611 vibrio para
1029	6	2.2	607	1	ALB2_XENIA	P14872 xenopus lae	502	6	2.2	839	1	TOPI_SYPN7	P34185 synechococc
1030	6	2.2	607	1	ALB2_XANCV	P80151 xanthomonas	503	6	2.2	841	1	CHSI_PHYBL	P87073 phycococc
1031	6	2.2	607	1	PEPF_MYCEG	P47429 mycoplasma	504	6	2.2	844	1	DNL4_HUMAN	P49917 rattus norv
1032	6	2.2	609	1	FETA_HORSE	P49066 equus caball	505	6	2.2	845	1	DNL4_HUMAN	P43244 rattus norv
1033	6	2.2	611	1	GIDA_MYCPU	Q98QV8 mycoplasma	506	6	2.2	847	1	MAT3_HUMAN	P43243 homo sapien
1034	6	2.2	611	1	PEPF_MYCPN	P54125 mycoplasma	507	6	2.2	848	1	CLPB_MYCTU	O53719 mycobacteri
1035	6	2.2	614	1	GLMS_STROC	O86781 s glucosami	508	6	2.2	853	1	CNBR_BOVIN	P23439 bos taurus
1036	6	2.2	614	1	YONK_LACIC	P42377 lactococcus	509	6	2.2	853	1	TOPI_BUCAP	Q8K9P7 bucherna ap
1037	6	2.2	618	1	CAB2_METUA	Q58776 methanococc	510	6	2.2	854	1	CNBR_HUMAN	P35913 homo sapien
1038	6	2.2	618	1	BCHD_CHLVI	O50313 chlorobium	511	6	2.2	856	1	CLPB_HABIN	P44403 haemophilus
1039	6	2.2	619	1	REL_HUMAN	Q04864 homo sapien	512	6	2.2	861	1	MVP_MOUSE	Q9eqk5 mus musculu
1040	6	2.2	620	1	BCHD_CHLTE	Q93sw0 chlorobium	513	6	2.2	866	1	PDG3_ARATH	Q9t052 arabidopsis
1041	6	2.2	621	1	ASPA_AERSA	P31339 aeromonas s	514	6	2.2	866	1	RECE_ECOLI	P15032 escherichia
1042	6	2.2	621	1	SRPR_YEAST	P32916 saccharomys	515	6	2.2	871	1	UL47_HSVEB	P28929 equine herp
1043	6	2.2	623	1	GLMS_MYCTU	O60253 m glucosami	516	6	2.2	872	1	CLPB_SINY3	P74361 synechocyst
1044	6	2.2	624	1	GLMS_MYCLE	P40831 m glucosami	517	6	2.2	884	1	SYA_RALSO	Q8Y193 ralstonia s
1045	6	2.2	625	1	SVR_SULSO	O97zn1 sulfolobus	518	6	2.2	887	1	SYA_AGRT5	Q8ue87 agrobacteri
1046	6	2.2	627	1	GLMS_MYCSM	O68956 m glucosami	519	6	2.2	889	1	IREB_CHICK	Q90875 gallus gall
1047	6	2.2	633	1	SNF1_YEAST	P06782 saccharomyc	520	6	2.2	892	1	RA16_SCHPO	P36617 schizosacch
1048	6	2.2	636	1	PTHS_SPIOL	P28723 spinacia ol	521	6	2.2	893	1	MVP_HUMAN	Q14764 homo sapien
1049	6	2.2	656	1	UYEL_NEURC	O01408 neurospora	522	6	2.2	898	1	ACOC_CUCMA	P49608 cucurbita m
1050	6	2.2	659	1	SP22_SINY3	P72587 synechocyst	523	6	2.2	899	1	VL20_HSVSA	Q01055 herpesvitr
1051	6	2.2	662	1	VELF_CDOV	P12569 canine dist	524	6	2.2	901	1	SOKI_YEAST	P40317 saccharomyc
1052	6	2.2	663	1	AE31_MOUSE	Q92887 mus musculu	525	6	2.2	902	1	ITHI_PIG	Q29052 sus scrofa
1053	6	2.2	663	1	OTRA_STRRM	P55002 streptomyce	526	6	2.2	907	1	ITHI_MOUSE	Q61702 mus musculu
1054	6	2.2	663	1	Y4MW_RHISN	P55691 rhizobium s	527	6	2.2	907	1	IGRS_HUMAN	Q75473 homo sapien
1055	6	2.2	666	1	VOOI_VARY	P34010 variola vir	528	6	2.2	911	1	ITHI_HUMAN	P15827 homo sapien
1056	6	2.2	668	1	DNLJ_BACSU	O31498 bacillus su	529	6	2.2	917	1	CTNA_DROME	P35220 drosophila
1057	6	2.2	669	1	ENGL_SINY3	Q55421 synechocyst	530	6	2.2	927	1	CC15_SCHPO	Q05822 schizosacch
1058	6	2.2	677	1	PTGA_CORGL	Q45298 corynebacte	531	6	2.2	928	1	DNL1_CANAL	P5x496 candida alb
1059	6	2.2	677	1	FXPI_HUMAN	Q9h334 homo sapien	532	6	2.2	929	1	DPOM_MAIZE	P10582 zea mays
1060	6	2.2	683	1	PTNA_CORGL	Q46072 corynebacte	533	6	2.2	934	1	CITC_HUMAN	P11586 h c-i-tetra
1061	6	2.2	687	1	FHSR_EQUAS	Q95179 equus asinu	534	6	2.2	934	1	CITC_RAT	P27653 r c-i-tetra
1062	6	2.2	693	1	GUAA_HUMAN	P49915 homo sapien	535	6	2.2	938	1	CITC_RAT	P23914 bacillus su
1063	6	2.2	694	1	HAAL_YEAST	Q12753 saccharomyc	536	6	2.2	944	1	LEVR_BACSU	P55972 helicobacte
1064	6	2.2	697	1	SRP_CAEEL	P41848 caenorhabdi	537	6	2.2	944	1	IF2_HELPJ	Q9sm46 helicobacte
1065	6	2.2	699	1	E75_MANSE	Q08893 manduca sex	538	6	2.2	949	1	IF2_HELPJ	Q9sm46 helicobacte
1066	6	2.2	705	1	FXPI_MOUSE	P58462 mus musculu	539	6	2.2	960	1	OPAI_HUMAN	O60313 homo sapien
1067	6	2.2	709	1	NU5C_PACQA	Q9mvk2 pachira agu	540	6	2.2	960	1	OPAI_MOUSE	P58281 mus musculu
1068	6	2.2	714	1	ATKB_MYCEG	P47597 mycoplasma	541	6	2.2	972	1	CSEI_ARATH	Q9zpy7 arabidopsis
1069	6	2.2	718	1	ATKB_AGRT5	Q8u9d9 agrobacteri	542	6	2.2	974	1	PODJ_CAUCR	Q95988 caulobacter
1070	6	2.2	718	1	PLSB_CAEEL	Q22949 caenorhabdi	543	6	2.2	994	1	FIBP_ADEB3	Q03553 bovine aden
1071	6	2.2	721	1	THIC_SHEON	Q8eed7 shewanella	544	6	2.2	994	1	ATA1_CHICK	P31585 r sarcoplas
	6	2.2	721	1			545	6	2.2			ATA1_RANES	Q92105 r sarcoplas



545	6	2.2	997	1	ATA2_CANPA	O46674	c sarcoplas	618	6	2.2	1938	1	MYSD_CABEL	P02567	caenorhabdi
546	6	2.2	997	1	ATA2_FELCA	Q00779	f sarcoplas	619	6	2.2	1947	1	MYSC_CABEL	P12845	caenorhabdi
547	6	2.2	998	1	RRPO_BBV	Q96631	black beetl	620	6	2.2	1962	1	MYSA_DROME	P05661	drosophila
548	6	2.2	998	1	RRPO_FHV	Q66929	flock house	621	6	2.2	1966	1	MYSB_CABEL	P02566	caenorhabdi
549	6	2.2	999	1	ATA3_RAT	P18596	rattus norv	622	6	2.2	1969	1	MYSA_CABEL	P12844	caenorhabdi
550	6	2.2	999	1	MFD_HELPY	Q26066	helicobacte	623	6	2.2	2130	1	BA2B_CHICK	Q9d13	gallus gall
551	6	2.2	1007	1	CHC2_HUMAN	Q9514	homo sapien	624	6	2.2	2210	1	RRPL_EBOSM	Q68002	ebola virus
552	6	2.2	1014	1	ODO1_YEAST	P20967	saccharomyc	625	6	2.2	2514	1	POLN_ONNVG	P13886	o'nyong-nyo
553	6	2.2	1027	1	CARY_BACSU	P18185	bacillus su	626	6	2.2	2542	1	TLN2_HUMAN	Q9y496	homo sapien
554	6	2.2	1033	1	YD56_SCHPO	O10309	schizosacch	627	6	2.2	2647	1	FLNA_HUMAN	P21333	homo sapien
555	6	2.2	1035	1	DROL_RHOM6	O71121	rhesus cyto	628	6	2.2	2713	1	CHD5_HUMAN	Q8td26	homo sapien
556	6	2.2	1038	1	ATA3_MOUSE	Q64518	mus musculus	629	6	2.2	2960	1	AHMK_HUMAN	Q99666	homo sapien
557	6	2.2	1040	1	YEGN_ECOLI	P76398	escherichia	630	6	2.2	3388	1	POLG_DEN2P	P12823	d genome po
558	6	2.2	1041	1	ATA2_CHICK	Q03669	g sarcoplas	631	6	2.2	3391	1	POLG_DEN26	P29990	d genome po
559	6	2.2	1041	1	EGT2_YEAST	P42835	saccharomyc	632	6	2.2	3391	1	POLG_DEN27	P29991	d genome po
560	6	2.2	1042	1	ATA2_HUMAN	P16615	h sarcoplas	633	6	2.2	3391	1	POLG_DEN2J	P07564	d genome po
561	6	2.2	1042	1	ATA2_PIG	P11607	s sarcoplas	634	6	2.2	3391	1	POLG_DEN2N	P14340	d genome po
562	6	2.2	1042	1	ATA2_RABIT	P20647	o sarcoplas	635	6	2.2	3801	1	LYST_HUMAN	Q99698	homo sapien
563	6	2.2	1042	1	ATA3_CHICK	Q9y919	gallus gall	636	6	2.2	4036	1	RRPL_DUGBV	Q66431	dugbe virus
564	6	2.2	1043	1	ATA2_RAT	P11507	r sarcoplas	637	6	2.2	4349	1	FAT2_HUMAN	Q9nyq8	homo sapien
565	6	2.2	1044	1	ATA2_MOUSE	O55143	m sarcoplas	638	6	2.2	4427	1	PKSL_BACSU	Q05470	bacillus su
566	6	2.2	1054	1	CYPE_BACSU	O08336	bacillus su	639	6	2.2	4447	1	PKSK_BACSU	P40803	bacillus su
567	6	2.2	1064	1	CARB_EACST	O50302	bacillus st	640	6	2.2	4563	1	APB_HUMAN	P04114	homo sapien
568	6	2.2	1065	1	CARB_BACCL	P46537	bacillus ca	641	6	2.2	5938	1	MAC4_HUMAN	Q96pk2	homo sapien
569	6	2.2	1065	1	NOLG_RHIME	P25197	rhizobium m	642	5	1.8	15	1	DIDH_PSESP	P80701	pseudomonas
570	6	2.2	1066	1	HVSA_STRPN	Q54873	streptococc	643	5	1.8	18	1	YMDB_CHIAU	Q45827	chloroflexu
571	6	2.2	1067	1	CARB_CLOPE	O8xhb3	clostridium	644	5	1.8	33	1	ALOX_PICPA	P04842	pchia past
572	6	2.2	1071	1	CARB_BACSU	P25994	bacillus su	645	5	1.8	42	1	YPI_EPPED	P27386	bacterioph
573	6	2.2	1072	1	SYIC_YEAST	P09436	saccharomyc	646	5	1.8	46	1	LHA1_ECTHA	P80100	ectothiorho
574	6	2.2	1074	1	PLD1_HUMAN	Q13393	homo sapien	647	5	1.8	47	1	LHA2_ECTHA	P80101	ectothiorho
575	6	2.2	1076	1	CARB_EUCEP	P59448	buchnera ap	648	5	1.8	47	1	Y311_TREPA	O83333	treponema p
576	6	2.2	1076	1	IF3A_CABEL	P34339	caenorhabdi	649	5	1.8	49	1	RPOP_PYRAB	Q9v201	pyrococcus
577	6	2.2	1076	1	NUPI_YEAST	P20676	saccharomyc	650	5	1.8	49	1	RPOP_PYRFU	O8tzi3	pyrococcus
578	6	2.2	1088	1	KGP2_DROME	Q03043	drosophila	651	5	1.8	49	1	RPOP_PYRHO	O4105	pyrococcus
579	6	2.2	1099	1	CARB_THENA	Q9wz27	thermotoga	652	5	1.8	54	1	AMAI_ALLMI	P40641	alligator m
580	6	2.2	1102	1	MYSC_CHICK	P29616	gallus gall	653	5	1.8	55	1	YHFG_ECOLI	P37770	escherichia
581	6	2.2	1103	1	CHS6_USTMA	O13395	ustilago ma	654	5	1.8	55	1	YHFG_SALTY	P37771	salmonella
582	6	2.2	1115	1	YAA4_SCHPO	Q09798	schizosacch	655	5	1.8	58	1	ATP6_BRATO	Q11721	brassicac to
583	6	2.2	1121	1	YEO6_YEAST	P32644	saccharomyc	656	5	1.8	59	1	SAKA_LACSK	P80097	lactobacill
584	6	2.2	1182	1	RTP2_TRYBG	P15594	trypanosoma	657	5	1.8	60	1	HNEN_LAMPL	P15334	lampetra pl
585	6	2.2	1191	1	SMC2_MOUSE	Q8c948	mus musculus	658	5	1.8	60	1	RS14_MYCCA	P10130	mycoplasma
586	6	2.2	1193	1	YFBR_BACSU	P54159	bacillus su	659	5	1.8	60	1	YH05_VACCV	P17356	vaccinia vi
587	6	2.2	1197	1	SMC2_HUMAN	Q95347	homo sapien	660	5	1.8	61	1	143X_MAIZE	P29306	zea mays (m
588	6	2.2	1203	1	SMC2_XENLA	P50533	xenopus lae	661	5	1.8	61	1	SUIS_PIG	P56729	sus scrofa
589	6	2.2	1214	1	SIP1_HUMAN	O60315	homo sapien	662	5	1.8	62	1	Y12D_BPT4	P39496	bacterioph
590	6	2.2	1215	1	SIP1_MOUSE	Q9r097	mus musculus	663	5	1.8	63	1	CE3G_HYPCU	P50723	hyphantria
591	6	2.2	1224	1	COPA_BOVIN	Q27954	bos taurus	664	5	1.8	63	1	COW3_CONTE	Q9nda6	conus texti
592	6	2.2	1248	1	TOPG_SULAC	Q08582	sulfolobus	665	5	1.8	63	1	COW_CONRA	P58786	conus radia
593	6	2.2	1265	1	RPOD_CYAPA	P48120	cyanophora	666	5	1.8	64	1	FABP_ACASI	O76821	acarus siro
594	6	2.2	1283	1	OSH2_YEAST	Q12451	saccharomyc	667	5	1.8	64	1	PHYB_PHYBI	P81565	phyllomedus
595	6	2.2	1367	1	LT23_CABEL	P24348	caenorhabdi	668	5	1.8	66	1	YQ23_BACAN	Q9rn09	bacillus an
596	6	2.2	1416	1	BLM_MOUSE	O88700	mus musculus	669	5	1.8	67	1	CERC_CERCA	Q17313	ceratitis c
597	6	2.2	1427	1	ZFH2_HUMAN	Q9c0a1	homo sapien	670	5	1.8	67	1	CSPB_BACSU	P32081	bacillus su
598	6	2.2	1428	1	YA84_SCHPO	Q09773	schizosacch	671	5	1.8	67	1	HM1_CHICK	P13544	gallus gall
599	6	2.2	1432	1	WRN_HUMAN	Q14191	homo sapien	672	5	1.8	68	1	YOR3_FIVSD	P19031	feline immu
600	6	2.2	1436	1	WRN_XENLA	Q91530	xenopus lae	673	5	1.8	69	1	RM39_YEAST	P36533	saccharomyc
601	6	2.2	1451	1	AT7B_RAT	Q64535	rattus norv	674	5	1.8	70	1	Y05Q_BPT4	P13305	bacterioph
602	6	2.2	1460	1	N159_YEAST	P40477	saccharomyc	675	5	1.8	70	1	Y535_TREPA	Q83546	treponema p
603	6	2.2	1462	1	AT7B_MOUSE	Q64446	mus musculus	676	5	1.8	71	1	YS30_RALSO	Q8xvko	raistonia s
604	6	2.2	1478	1	BUD3_ASHGO	Q9hf61	ashbya goss	677	5	1.8	73	1	BB13_SCHCO	P78744	schizophyll
605	6	2.2	1559	1	STCJ_EMENI	Q00681	emeritella	678	5	1.8	73	1	GEPA_BACSU	O06721	bacillus su
606	6	2.2	1574	1	RPOC_AQUAE	O67763	aquifex aeo	679	5	1.8	73	1	IF1_CHLPN	Q9z9a8	chlamydia p
607	6	2.2	1576	1	RPOC_AQUUPY	Q9x6y2	aquifex pyr	680	5	1.8	73	1	PEPG_PIG	P30879	sus scrofa
608	6	2.2	1581	1	PRRB_HUMAN	Q15648	h peroxisom	681	5	1.8	74	1	CIM_BPMU	P30046	bacterioph
609	6	2.2	1658	1	ITN2_MOUSE	Q9z0r6	mus musculus	682	5	1.8	74	1	HOLI_BPDP1	Q03978	bacterioph
610	6	2.2	1677	1	VIT_ACTR	Q90243	acipenser t	683	5	1.8	74	1	UL11_HSVBP	P28982	equine herp
611	6	2.2	1696	1	ITN2_HUMAN	Q9nzm3	homo sapien	684	5	1.8	74	1	Y11B_BPT4	P32281	bacterioph
612	6	2.2	1714	1	SVEP_DROME	P28668	drosophila	685	5	1.8	74	1	Y4HR_RHFSN	P55482	rhizobium s
613	6	2.2	1739	1	DOTL_HUMAN	Q8tek3	homo sapien	686	5	1.8	74	1	YD97_CAMJE	Q9pmr0	campylobact
614	6	2.2	1744	1	TANA_XENLA	Q01550	xenopus lae	687	5	1.8	75	1	RL31_BRAJA	Q89ub0	bradyrhizob
615	6	2.2	1807	1	TSC2_HUMAN	P49815	homo sapien	688	5	1.8	76	1	ACP_OCELI	P09022	oceanospiri
616	6	2.2	1808	1	TENA_CHICK	P10039	gallus gall	689	5	1.8	76	1	CD24_MOUSE	P24807	mus musculus
617	6	2.2	1809	1	TSC2_RAT	P49816	rattus norv	690	5	1.8	76	1	RL31_CAUCR	Q9a3c9	caulobacter

P02567	caenorhabdi
P12845	caenorhabdi
P05661	drosophila
P02566	caenorhabdi
P12844	caenorhabdi
Q9d13	gallus gall
Q68002	ebola virus
P13886	o'nyong-nyo
Q9y496	homo sapien
P21333	homo sapien
Q8td26	homo sapien
Q99666	homo sapien
P12823	d genome po
P29990	d genome po
P29991	d genome po
P07564	d genome po
P14340	d genome po
Q99698	homo sapien
Q66431	dugbe virus
Q9nyq8	homo sapien
Q05470	bacillus su
P40803	bacillus su
P04114	homo sapien
Q96pk2	homo sapien
P80701	pseudomonas
Q45827	chloroflexu
P04842	pchia past
P27386	bacterioph
P80100	ectothiorho
P80101	ectothiorho
O83333	treponema p
Q9v201	pyrococcus
O8tzi3	pyrococcus
Q74105	pyrococcus
P40641	alligator m
P37770	escherichia
F37771	salmonella
K31721	brassica to
P80097	lactobacill
P31534	lampetra pl
P10130	mycoplasma
P17356	vaccinia vi
P29306	zea mays (m
P56729	yeast scrofa
P34936	bacterioph
P50723	hyphantria
Q9nda6	conus texti
F58786	conus radiat
O76821	acarus siro
P81565	phyllostedus
Q9rm09	bacillus an
Q17313	ceratitis c
P32081	batillus su
P13544	gallus gall
P19031	feline immu
P36533	saccharomy
P13305	bacterioph
O83546	treponema p
Q8xvk0	raistonis s
P78744	schizophyll
O06721	bacillus su
Q92948	chlamydia p
P30879	yeast scrofa
O03046	bacterioph
O03978	bacterioph
F28982	equine herp
P32281	bacterioph
P55482	rhibobium s
Q9pmr0	campylobact
Q89u30	bradyrhizob
O80922	oceanospiri
P24807	yeast musculu
Q9a369	caulobacter

691	1	1.8	76	1	TATA_PASMU	Q9ckd3	pasteurella	764	5	1.8	96	1	VE7_HPV24	P50782	human papill
692	1	1.8	77	1	ACP1_PSEAE	Q54439	pseudomonas	765	5	1.8	97	1	7E_DICD1	P15649	dictyosteli
693	1	1.8	77	1	ACP_PSEEM	P90923	pseudomonas	766	5	1.8	97	1	CH10_ACEAC	Q9gbd3	acetobacter
694	1	1.8	77	1	XG5_CLOAB	Q97hd1	clostridium	767	5	1.8	97	1	YF51_HELPF	Q9zj67	helicobacte
695	1	1.8	77	1	TEGP_SVVD	Q45446	simian vari	768	5	1.8	98	1	CYTA_HUMAN	P01040	homo sapien
696	1	1.8	78	1	ACP_XANAC	P58986	xanthomonas	769	5	1.8	98	1	FIXX_RHIME	P09822	thizobium m
697	1	1.8	78	1	ACP_XANAL	Q9ez11	xanthomonas	770	5	1.8	98	1	P531_MOUSE	P70399	mus musculus
698	1	1.8	78	1	RLX_PYRAF	Q9ztu0	pyrobaculum	771	5	1.8	98	1	Z126_HUMAN	P35275	homo sapien
699	1	1.8	78	1	UGL3_AMEPV	P29819	amsacta moo	772	5	1.8	99	1	ARG2_PHAU	P32292	phaseolus a
700	1	1.8	79	1	CSNA_CHLTE	Q46467	chlorobium	773	5	1.8	99	1	HG14_HUMAN	P05114	homo sapien
701	1	1.8	79	1	RPOZ_THEMA	Q9x214	thermotoga	774	5	1.8	99	1	PCP2_HUMAN	Q91741	homo sapien
702	1	1.8	79	1	TATA_HELPF	Q9zmb8	helicobacte	775	5	1.8	99	1	Y107_MICTU	Q50718	mycobacteri
703	1	1.8	79	1	YF51_CAEEL	Q17811	caenorhabdi	776	5	1.8	100	1	HG14_BOVIN	P02316	bos taurus
704	1	1.8	80	1	CD24_HUMAN	P25063	homo sapien	777	5	1.8	100	1	URE3_BORBR	P06705	bordetella
705	1	1.8	80	1	RUXG_ARATH	O82221	arabidopsis	778	5	1.8	100	1	URE3_LACFE	P26931	lactobacill
706	1	1.8	81	1	ATPL_CLOAB	O08310	clostridium	779	5	1.8	100	1	URE3_STRSL	Q55053	streptococc
707	1	1.8	81	1	RUXG_MEDSA	P24715	medicago sa	780	5	1.8	100	1	YH74_ARCFU	O28520	archaeoglob
708	1	1.8	81	1	Y65_BPT3	P20329	bacterioph	781	5	1.8	101	1	TULC_MAIZE	P11646	zea mays (m
709	1	1.8	81	1	CSGA_BACSU	P54379	bacillus su	782	5	1.8	101	1	NUHB_PHOSU	Q62590	phodopus su
710	1	1.8	82	1	S61B_ARATH	P38389	arabidopsis	783	5	1.8	101	1	URE3_UREPA	Q56557	ureaplasma
711	1	1.8	82	1	Y070_METUA	Q60373	methanococc	784	5	1.8	101	1	VATF_ARCFU	P17274	ureaplasma
712	1	1.8	82	1	Y9XD_BPCHP	P19191	bacterioph	785	5	1.8	101	1	VNS7_CVFE3	O29102	archaeoglob
713	1	1.8	83	1	COXJ_HUMAN	P14406	homo sapien	786	5	1.8	101	1	VNS7_CVFE3	P33465	feline ente
714	1	1.8	83	1	GVZ2_HALNI	P33960	halobacteri	787	5	1.8	101	1	VNS7_FIPV	P19742	feline infe
715	1	1.8	83	1	Y405_ARCFU	O29842	archaeoglob	788	5	1.8	102	1	IFPB_AGRU	O52514	agrobacteri
716	1	1.8	83	1	YCIN_ECOLI	P46132	escherichia	789	5	1.8	102	1	RS10_CLOAB	Q97eh7	clostridium
717	1	1.8	83	1	YF24_ARCFU	O28748	archaeoglob	790	5	1.8	102	1	RS10_PLARO	P72232	human bispor
718	1	1.8	83	1	HEFC_RAT	Q99m43	rattus norv	791	5	1.8	102	1	VE7_HPV19	P36822	human papill
719	1	1.8	84	1	CY6_PETFA	P00108	petalonia f	792	5	1.8	102	1	VCES_BPDI0	P08795	bacterioph
720	1	1.8	85	1	UG13_HSVL0	P24439	human herpe	793	5	1.8	102	1	CEAV_ECOLI	P25522	escherichia
721	1	1.8	85	1	VG73_BFVL5	Q52888	mycobacteri	794	5	1.8	103	1	EMF1_CHICK	P08317	gallus gall
722	1	1.8	85	1	Y070_METUA	Q97683	methanococc	795	5	1.8	103	1	HIS2_RHOA	Q50935	rhodobacter
723	1	1.8	86	1	CY6_ALAES	P00109	alarial escu	796	5	1.8	103	1	HIS2_RHOA	P50935	rhodobacter
724	1	1.8	86	1	CY6_BUMFI	P00110	bulleriosis	797	5	1.8	103	1	LAC_CHICK	P20763	gallus gall
725	1	1.8	87	1	ANSA_STRCZ	P01548	streptomyce	798	5	1.8	103	1	NRAM_TACAO	P26143	influenza a
726	1	1.8	87	1	HEB_DASVI	P07420	dasyurus vi	799	5	1.8	103	1	OST4_PIG	Q29381	sus scrofa
727	1	1.8	87	1	NUOS_HUMAN	Q9nrx3	homo sapien	800	5	1.8	103	1	YCX2_CHLEY	P05721	chlorella p
728	1	1.8	87	1	RS20_CORGL	Q9nn66	corynebacte	801	5	1.8	103	1	YATF_THEVO	Q97cql	thermoplasm
729	1	1.8	87	1	RS20_NEIMA	Q97683	methanococc	802	5	1.8	104	1	Y4EB_RHISN	P55425	thizobium s
730	1	1.8	87	1	Y230_METUA	P36549	bacillus li	803	5	1.8	104	1	PSBX_SOYBN	Q02921	glycine max
731	1	1.8	87	1	YAF2_BACLI	P46477	escherichia	804	5	1.8	105	1	PSBX_GOSHI	P31336	gossypium h
732	1	1.8	87	1	YHNC_ECOLI	P43740	haemophilus	805	5	1.8	105	1	C07S_HUMAN	O60397	homo sapien
733	1	1.8	88	1	RPOZ_HAEIN	O51744	borrelia bu	806	5	1.8	106	1	KACB_RABIT	P01839	oryctolagus
734	1	1.8	88	1	RS15_BORBU	Q91744	borrelia bu	807	5	1.8	106	1	KACB_RAT	P01835	rattus norv
735	1	1.8	89	1	FLIQ_BUCAI	P57185	buchnera ap	808	5	1.8	106	1	KACB_HUMAN	P01834	homo sapien
736	1	1.8	89	1	NRAM_TAMEI	P03471	influenza a	809	5	1.8	106	1	VATF_HALVO	Q48331	halobacteri
737	1	1.8	89	1	SDP1_MOUSE	P40224	mus musculus	810	5	1.8	106	1	Y547_RICPR	Q9zd03	rickettsia
738	1	1.8	89	1	VP54_BPAPS	O9t154	bacterioph	811	5	1.8	106	1	YB07_YEAST	P38284	saccharomyc
739	1	1.8	89	1	YF19_MYCTU	Q50588	mycobacteri	812	5	1.8	106	1	YVBB_VACC	P20554	vaccinia vi
740	1	1.8	90	1	BAPL_DROME	Q9vlu0	drosophila	813	5	1.8	106	1	HIS2_RHIL0	Q98c00	thizobium l
741	1	1.8	90	1	DMFM_FRESP	P19731	pseudomonas	814	5	1.8	107	1	YB11_BACHD	Q9kdv0	bacillus ha
742	1	1.8	90	1	MODL_SYNPF	Q96209	synchococc	815	5	1.8	107	1	GLPE_ECO57	Q8x625	escherichia
743	1	1.8	90	1	RPOL_SULAC	P46217	sulfolobus	816	5	1.8	108	1	GLPE_ECOLI	P09390	escherichia
744	1	1.8	90	1	Y071_METUA	Q60374	methanococc	817	5	1.8	108	1	GLPE_SALTY	Q9xf66	salmonella
745	1	1.8	90	1	YEAC_ECOLI	P76231	escherichia	818	5	1.8	108	1	HIS3_ARCFU	O28329	archaeoglob
746	1	1.8	92	1	ACYP_ECOLI	P75877	escherichia	819	5	1.8	108	1	INS_PIG	P01315	sus scrofa
747	1	1.8	92	1	RK23_MESVI	Q9mt8	mesostigma	820	5	1.8	108	1	PRVB_RANES	P02617	rana escul
748	1	1.8	92	1	YC23_METUA	Q58620	methanococc	821	5	1.8	108	1	Y388_MYCPN	P75209	mycoplasma
749	1	1.8	93	1	COM6_NEUCR	P34762	neurospora	822	5	1.8	108	1	YGLB_BACST	P30540	bacillus st
750	1	1.8	93	1	HIS2_MYCLE	Q49786	mycobacteri	823	5	1.8	108	1	CY66_CYACA	Q9t1w1	cyanidium c
751	1	1.8	93	1	HIS2_MYCTU	O33257	mycobacteri	824	5	1.8	109	1	GLPE_YERPE	Q8zj13	yersinia pe
752	1	1.8	93	1	RS16_CANTP	Q9kte4	canidatus	825	5	1.8	109	1	GLPM_PSEAE	P52112	pseudomonas
753	1	1.8	93	1	SDP1_FELCA	O62657	felis silve	826	5	1.8	109	1	SZ13_MOUSE	Q55038	mus musculus
754	1	1.8	93	1	INPB_RHOCA	P42030	rhodobacter	827	5	1.8	109	1	YMW3_MYCTU	Q50690	mycobacteri
755	1	1.8	94	1	IFPB_BRUME	Q9vet3	bruceella me	828	5	1.8	109	1	RLA4_YEAST	P02400	saccharomyc
756	1	1.8	94	1	SV17_HUMAN	Q52583	homo sapien	829	5	1.8	110	1	THIO_EUBAC	P21610	eubacterium
757	1	1.8	94	1	VG41_BPMDO	Q64231	mycobacteri	830	5	1.8	110	1	VCAD_LAMB	P03712	bacterioph
758	1	1.8	94	1	Y753_TREPA	O93714	treponema p	831	5	1.8	110	1	Y484_RICPR	Q9zjd62	rickettsia
759	1	1.8	94	1	YQVY_BACSU	P54499	baicallus au	832	5	1.8	110	1	HIS2_AZORR	P26722	azospirilla
760	1	1.8	95	1	ACOX_STRSM	P43677	streptomyce	833	5	1.8	111	1	IFM1_METAC	Q8tea3	methanosarc
761	1	1.8	95	1	ATPJ_YEAST	P81449	saccharomyc	834	5	1.8	111	1	IFM1_METWA	Q9pyf1	methanosarc
762	1	1.8	95	1	NCCY_ALCAX	Q44581	alcaligenes	835	5	1.8	111	1	RL22_CHLMU	Q9fj19	chlamydia m
763	1	1.8	96	1	CNRY_ALCEU	P56621	alcaligenes	836	5	1.8	111	1			

837	5	1.8	111	1	RL22_CHLTR	084528 chlamydia t	910	5	1.8	121	1	GLN2_METTM	Q50787 methanobact
838	5	1.8	111	1	RLA2_ASPEU	Q9uuz6 aspergillus	911	5	1.8	121	1	LCA_MACRG	P07458 macropus ru
839	5	1.8	111	1	RLP134_XANAC	Q8pi34 xanthomonas	912	5	1.8	121	1	PUCM_BACSU	Q32142 bacillus su
840	5	1.8	112	1	GLNB_RHIET	O54053 rhizobium e	913	5	1.8	121	1	R18E_METTH	Q36145 methanobact
841	5	1.8	112	1	GLNK_ECOLI	P38504 escherichia	914	5	1.8	121	1	RBPA_CLOAB	Q37150 clostridium
842	5	1.8	112	1	SECG_HAEIN	P44713 haemophilus	915	5	1.8	121	1	RK14_CYACA	Q9tlu2 cyanidium c
843	5	1.8	112	1	SHP_RHOSH	P81238 rhodobacter	916	5	1.8	121	1	Y621_PYRAB	Q9v108 pyrococcus
844	5	1.8	112	1	THL_CLODI	P45362 clostridium	917	5	1.8	121	1	YGIW_HAEIN	P44293 haemophilus
845	5	1.8	112	1	YC83_GALSU	Q9msa1 galdieria s	918	5	1.8	122	1	RL14_MARPO	P06381 marchantia
846	5	1.8	113	1	H38_STYLE	RL1202 stylonychia	919	5	1.8	122	1	RL14_MYCCA	P10137 mycoplasma
847	5	1.8	113	1	NLTI_WHEAT	P24295 triticum ae	920	5	1.8	122	1	TRJ6_ECOLI	P17903 escherichia
848	5	1.8	113	1	RBPA_LACLC	Q9x765 lactococcus	921	5	1.8	122	1	Y284_MYCPN	P17909 mycoplasma
849	5	1.8	113	1	Y068_METMP	Q9p9e9 methanococc	922	5	1.8	122	1	Y303_AGRTS	Q8uij2 agrobacteri
850	5	1.8	113	1	YAB1_THEMA	Q9x0h0 thermotoga	923	5	1.8	122	1	YFV6_METTF	P29580 methanobact
851	5	1.8	113	1	YAB1_THEMA	O86949 thermotoga	924	5	1.8	122	1	YFV6_METTF	P29581 methanobact
852	5	1.8	113	1	YJ52_YEAST	P47128 saccharomyc	925	5	1.8	122	1	ELI2_PHYCR	P41803 phytophthor
853	5	1.8	114	1	GTH1_FUNHE	P30971 fundulus he	926	5	1.8	123	1	ELI2_PHYCR	P41804 phytophthor
854	5	1.8	114	1	H31_STYLE	P81195 stylonychia	927	5	1.8	123	1	RS11_MYCPE	P59372 mycoplasma
855	5	1.8	114	1	H35_STYLE	P81197 stylonychia	928	5	1.8	123	1	Y003_FOMPV	Q9iccl1 fowlpox vir
856	5	1.8	114	1	H35_STYLE	P81199 stylonychia	929	5	1.8	123	1	YBAV_ECOLI	P77415 escherichia
857	5	1.8	114	1	H36_STYLE	P81200 stylonychia	930	5	1.8	123	1	CRCB_METJA	Q58918 methanococc
858	5	1.8	114	1	H37_STYLE	P81201 stylonychia	931	5	1.8	124	1	GCSH_HALN1	Q9hpi8 halobacteri
859	5	1.8	114	1	H39_STYLE	P81196 stylonychia	932	5	1.8	124	1	RS12_ERWAM	P45809 erwinia amy
860	5	1.8	114	1	MPFE_SAGOE	O97935 sagulinus oe	933	5	1.8	125	1	CRCB_RHIME	Q92qe1 rhizobium m
861	5	1.8	115	1	HV44_MOUSE	P01820 mus musculu	934	5	1.8	125	1	GDF6_MOUSE	P43028 mus musculu
862	5	1.8	115	1	NU3M_PONPA	P92697 pongo pygma	935	5	1.8	125	1	PLAS_SYNPT	P55020 synechococc
863	5	1.8	115	1	PT19_STYPL	P28211 styela plic	936	5	1.8	125	1	SDIS_COMTE	P00947 comanonas t
864	5	1.8	115	1	SECG_PASMU	Q9cp52 pasteurella	937	5	1.8	125	1	SECG_BORBU	O51083 borrelia bu
865	5	1.8	115	1	TIAP_HUMAN	O95411 homo sapien	938	5	1.8	126	1	CRB2_METAC	Q8tiq4 methanosarc
866	5	1.8	115	1	TIAP_MOUSE	Q9z194 mus musculu	939	5	1.8	126	1	CRB2_METAC	Q8pyn2 methanosarc
867	5	1.8	115	1	TKN1_RABIT	P16826 human cytom	940	5	1.8	126	1	LY6E_CHICK	Q90986 gallus gall
868	5	1.8	115	1	ULAI_HCMVA	P16826 human cytom	941	5	1.8	127	1	ACM2_BOVIN	P41985 bos taurus
869	5	1.8	115	1	Y128_TREPA	O83165 treponema p	942	5	1.8	127	1	CALI_HORSE	Q9n0t2 equus cabal
870	5	1.8	115	1	YIDD_MYCPA	Q917m0 mycobacteri	943	5	1.8	127	1	TRBC_RHLSN	P55396 rhizobium s
871	5	1.8	115	1	YNOB_PSEST	Q52528 pseudomonas	944	5	1.8	127	1	VB20_VACCC	P21078 vaccinia vi
872	5	1.8	115	1	YF88_MYCTU	Q50633 mycobacteri	945	5	1.8	127	1	YF51_HELPU	O36075 helicobact
873	5	1.8	116	1	CH15_DROVI	P13424 drosophila	946	5	1.8	127	1	YFFN_ECOLI	P76545 escherichia
874	5	1.8	116	1	NU3M_ONCGO	P20686 oncorhynch	947	5	1.8	128	1	IF5A_METAC	Q8tj03 methanosarc
875	5	1.8	116	1	NU3M_ONCKE	Q35262 oncorhynch	948	5	1.8	128	1	IF5A_METMA	O8pye0 methanosarc
876	5	1.8	116	1	NU3M_ONCKI	P20687 oncorhynch	949	5	1.8	128	1	Y097_BORBU	O51124 borrelia bu
877	5	1.8	116	1	NU3M_ONCWA	Q37108 oncorhynch	950	5	1.8	128	1	YPB3_CABEL	Q11106 caenorhabdi
878	5	1.8	116	1	NU3M_ONCNY	P11629 oncorhynch	951	5	1.8	129	1	RS8_ECOLI	P02361 escherichia
879	5	1.8	116	1	NU3M_ONCNE	P20688 oncorhynch	952	5	1.8	129	1	RS8_HAEIN	P44377 haemophilus
880	5	1.8	116	1	NU3M_ONCTS	P25707 oncorhynch	953	5	1.8	129	1	RT16_DROME	Q9v6y3 drosophila
881	5	1.8	116	1	NU3M_SALSA	Q35929 salmo salar	954	5	1.8	129	1	TDCF_ECOLI	P42631 escherichia
882	5	1.8	116	1	NU3M_SALTR	O03252 salmo trutt	955	5	1.8	129	1	VE11_VACCV	P21051 vaccinia vi
883	5	1.8	116	1	STP2_RAT	P11101 rattus norv	956	5	1.8	129	1	VE11_VARV	P33822 variola vir
884	5	1.8	116	1	TKNK_MOUSE	P55099 mus musculu	957	5	1.8	129	1	YM62_CHLTE	Q8kaa4 chlorobium
885	5	1.8	116	1	TKNK_RAT	P08435 rattus norv	958	5	1.8	130	1	DBH_UREPA	Q9pqk9 ureaplasma
886	5	1.8	116	1	YJ57_YEAST	P47132 saccharomyc	959	5	1.8	130	1	GLOV_HYACE	P81048 hyalophora
887	5	1.8	117	1	H1A1_DICDI	P13231 dictyosteli	960	5	1.8	130	1	RL22_CABEL	P52819 caenorhabdi
888	5	1.8	117	1	NTPF_ENTHR	P43437 enterococc	961	5	1.8	130	1	RNT1_ASPOR	P00651 aspergillus
889	5	1.8	117	1	VNEM_WCMVO	P15404 white clove	962	5	1.8	130	1	RS8_EUCAK	P46180 buchnera ap
890	5	1.8	117	1	VN01_VARV	P34018 variola vir	963	5	1.8	130	1	RS8_PASMU	Q9cl44 pasteurella
891	5	1.8	117	1	YIAB_ECOLI	P1286 escherichia	964	5	1.8	130	1	RS8_VIBCH	Q9knz8 vibrio chol
892	5	1.8	118	1	YRP3_IRV6	P18307 chilo iride	965	5	1.8	130	1	RS8_VIBPA	Q87sz9 vibrio para
893	5	1.8	118	1	YRP4_IRV6	P18308 chilo iride	966	5	1.8	130	1	RS8_VIBVU	Q8de54 vibrio vuln
894	5	1.8	119	1	ACPS_BACHD	Q8kfg1 bacillus ha	967	5	1.8	130	1	RS8_YERPE	Q8zj98 yersinia pe
895	5	1.8	119	1	BZMG_HUMAN	P01884 homo sapien	968	5	1.8	130	1	YB12_MYCPN	P75450 mycoplasma
896	5	1.8	119	1	BZMG_MACFA	Q8epw0 macaca fasc	969	5	1.8	130	1	YE65_AQUAE	O67445 aquifex aeo
897	5	1.8	119	1	BZMG_PONPY	P16213 pongo pygma	970	5	1.8	130	1	YHFU_ECOLI	P45547 escherichia
898	5	1.8	119	1	HEM1_PHAGO	P27686 phascolopsi	971	5	1.8	131	1	IL13_MOUSE	P20109 mus musculu
899	5	1.8	119	1	MP2_NERDI	P80255 nereis dive	972	5	1.8	131	1	IL13_RAT	P42203 rattus norv
900	5	1.8	119	1	RRFA_LACLA	Q8chg3 lactococcus	973	5	1.8	131	1	PER_ZAPTU	Q27135 zapronus t
901	5	1.8	120	1	HV2B_HUMAN	P01815 homo sapien	974	5	1.8	131	1	RS8_RALSO	Q8xv26 ralstonia s
902	5	1.8	120	1	NEUB_XENLA	P43443 xenopus lae	975	5	1.8	131	1	SPEH_THEAC	Q9hiy0 thermoplas
903	5	1.8	120	1	NU3C_SYNY3	P19045 synechocyst	976	5	1.8	131	1	STP2_BOVIN	P26377 bos taurus
904	5	1.8	120	1	RL18_SYNY3	P73305 synechocyst	977	5	1.8	131	1	T2RA_RAT	Q9ike8 rattus norv
905	5	1.8	120	1	RL7A_HALN1	Q9hqh8 halobacteri	978	5	1.8	131	1	YE98_AQUAE	O67469 aquifex aeo
906	5	1.8	120	1	VATF_HALN1	Q9hme2 halobacteri	979	5	1.8	131	1	YECN_ECOLI	P76289 escherichia
907	5	1.8	120	1	Y710_PYRAE	Q8zym4 pyrobaculum	980	5	1.8	132	1	DCUA_SERMA	P40684 serratia ma
908	5	1.8	120	1	Y555_PYRHO	O59124 pyrococcus	981	5	1.8	132	1	H2A_PLAFA	P40282 plasmodium
909	5	1.8	121	1	GLN2_METMP	P71525 methanococc	982	5	1.8	132	1	HVAE_ECOLI	P19931 escherichia

910	5	1.8	121	1	GLN2_METTM	Q50787 methanobact
911	5	1.8	121	1	LCA_MACRG	P07458 macropus ru
912	5	1.8	121	1	PUCM_BACSU	Q32142 bacillus su
913	5	1.8	121	1	R18E_METTH	Q26145 methanobact
914	5	1.8	121	1	RBPA_CLOAB	Q97150 clostridium
915	5	1.8	121	1	RK14_CYACA	Q9tlu2 cyanidium c
916	5	1.8	121	1	Y621_PYRAB	Q9v108 pyrococcus
917	5	1.8	121	1	YGIW_HAEIN	P44293 haemophilus
918	5	1.8	122	1	RL14_MARPO	P06381 marchantia
919	5	1.8	122	1	RL14_MYCCA	P10137 mycoplasma
920	5	1.8	122	1	TRJ6_ECOLI	P17903 escherichia
921	5	1.8	122	1	Y284_MYCPN	P17909 mycoplasma
922	5	1.8	122	1	Y303_AGRT5	Q8uij2 agrobacteri
923	5	1.8	122	1	YPV6_METTF	P29580 methanobact
924	5	1.8	122	1	YP26_METTF	P29581 methanobact
925	5	1.8	123	1	ELI2_PHYCR	P41803 phytophthor
926	5	1.8	123	1	ELI3_PHYCR	P41804 phytophthor
927	5	1.8	123	1	RS11_MYCPE	P59372 mycoplasma
928	5	1.8	123	1	Y003_FOMPV	Q9iccl1 fowlpox vir
929	5	1.8	123	1	YBAV_ECOLI	P77415 escherichia
930	5	1.8	124	1	CRCB_METJA	Q58918 methanococc
931	5	1.8	124	1	GCSH_HALN1	Q9hpi8 halobacteri
932	5	1.8	124	1	RS12_ERWAM	P45809 erwinia amy
933	5	1.8	125	1	CRCB_RHIME	Q92qe1 rhizobium m
934	5	1.8	125	1	GDF6_MOUSE	P43028 mus musculu
935	5	1.8	125	1	PLAS_SYNPT	P55020 synechococc
936	5	1.8	125	1	SDIS_COMTE	P00947 comamonas t
937	5	1.8	125	1	SECG_BORBU	O51083 borrelia bu
938	5	1.8	126	1	CRB2_METAC	Q8tiq4 methanosarc
939	5	1.8	126	1	CRB2_METMA	Q8pyn2 methanosarc
940	5	1.8	126	1	LY6E_CHICK	Q90986 gallus gall
941	5	1.8	127	1	ACM2_BOVIN	P41985 bos taurus
942	5	1.8	127	1	CALI_HORSE	Q9n0t2 equus cabal
943	5	1.8	127	1	TRBC_RHISN	P55396 rhizobium s
944	5	1.8	127	1	VB20_VACCC	P21078 vaccinia vi
945	5	1.8	127	1	YF51_HELPU	O26075 helicobacte
946	5	1.8	127	1	YFFN_ECOLI	P76545 escherichia
947	5	1.8	128	1	IF5A_METAC	Q8tj03 methanosarc
948	5	1.8	128	1	IF5A_METMA	O8pye0 methanosarc
949	5	1.8	128	1	Y097_BORBU	O51124 borrelia bu
950	5	1.8	128	1	YPB3_CAEEL	Q11106 caenorhabdi
951	5	1.8	129	1	RS8_ECOLI	P02361 escherichia
952	5	1.8	129	1	RS8_HAEIN	P44377 haemophilus
953	5	1.8	129	1	RT16_DROME	Q9v6y3 drosophila
954	5	1.8	129	1	TDCF_ECOLI	P42631 escherichia
955	5	1.8	129	1	VE11_VACCV	P21051 vaccinia vi
956	5	1.8	129	1	VE11_YARV	P33822 variola vir
957	5	1.8	129	1	YMG2_CHLTE	Q8kaa4 chlorobium
958	5	1.8	130	1	DBH_UREPA	Q9pqk9 ureaplasma
959	5	1.8	130	1	GLOV_HYACE	P81048 haenlophora
960	5	1.8	130	1	RL22_CAEEL	P52819 caenorhabdi
961	5	1.8	130	1	RNT1_ASPOR	P06651 aspergillus
962	5	1.8	130	1	RS8_EUCAK	P46180 buchnera ap
963	5	1.8	130	1	RS8_PASMU	Q9ci44 pasteurella
964	5	1.8	130	1	RS8_VIECH	Q9knz8 vibrio chol
965	5	1.8	130	1	RS8_VIEPA	Q87829 vibrio para
966	5	1.8	130	1	RS8_VIBVU	Q8de54 vibrio vuln
967	5	1.8	130	1	RS8_YERPE	Q82j98 yersinia pe
968	5	1.8	130	1	YB12_MYCPN	P75450 mycoplasma
969	5	1.8	130	1	YE65_AQUAE	O67445 aquifex aeo
970	5	1.8	130	1	YHFU_ECOLI	P45547 escherichia
971	5	1.8	131	1	IL13_MOUSE	P20109 mus musculu
972	5	1.8	131	1	IL13_RAT	P42203 rattus norv
973	5	1.8	131	1	PER_ZAPTU	Q27135 zapionus t
974	5	1.8	131	1	RS8_RALSO	Q8xv26 raistonia s
975	5	1.8	131	1	SPEH_THEAC	Q9hiy0 thermoplas
976	5	1.8	131	1	STP2_BOVIN	P26377 bos taurus
977	5	1.8	131	1	T2RA_RAT	Q9jke8 rattus norv
978	5	1.8	131	1	YE98_AQUAE	O67469 aquifex aeo
979	5	1.8	131	1	YECN_ECOLI	P76289 escherichia
980	5	1.8	132	1	DCUA_SERMA	P40684 serratia ma
981	5	1.8	132	1	H2A_PLAFA	P40282 plasmodium
982	5	1.8	132	1	HYAE_ECOLI	P19931 escherichia

983 1.8 132 1 NRDI\_AGR75 OQu69 agrobacteri  
984 1.8 132 1 RS8\_XANAC Q8pm3 xanthomonas  
985 1.8 132 1 RS8\_XANCP Q8pc38 xanthomonas  
986 1.8 132 1 Y284\_MYCGE P47526 mycoplasma  
987 1.8 133 1 Y4DO\_EHISN P5414 rhizobium s  
988 1.8 133 1 Y067\_CAEHL P34748 caenorhabdi  
989 1.8 134 1 CRB2\_EACHD Q9k819 bacillus ha  
990 1.8 134 1 CYB\_ANOCU Q31684 anoura card  
991 1.8 134 1 H3\_VOLUCA P08437 volvox cart  
992 1.8 134 1 NRDI\_YEREE Q8zdc6 yersinia pe  
993 1.8 134 1 TRBC\_AGRTE P54908 agrobacteri  
994 1.8 134 1 V22\_BPT5 P23541 bacterioph  
995 1.8 134 1 VC05\_VARV P34013 variola vir  
996 1.8 135 1 H31\_TETPY P15511 tetrahymena  
997 1.8 135 1 H3\_ACRFO P22843 acropora fo  
998 1.8 135 1 H3\_EUPCR P20543 euplotes cr  
999 1.8 135 1 NRDI\_BRUME Q8ybg9 bruceella me  
1000 1.8 135 1 YF84\_MYCPN P75196 mycoplasma

## ALIGNMENTS

RESULT 1  
LINK\_PSEPA STANDARD; PRT; 250 AA.  
ID LINK\_PSEPA STANDARD; PRT; 250 AA.  
AC P50198;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE 2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase (EC 1.1.-.-)  
DE (2,5-DDOL dehydrogenase).  
LNK.  
GN Pseudomonas paucimobilis (Sphingomonas paucimobilis).  
OS Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;  
OC Sphingomonadaceae; Sphingomonas.  
OX NCBI\_TaxID=13689;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=UT26;  
RX MEDLINE=94252977; PubMed=7515041;  
RA Nagata Y., Ohtomo R., Miyauchi K., Fukuda M., Yano K., Takagi M.;  
RT "Cloning and sequencing of a 2,5-dichloro-2,5-cyclohexadiene-1,4-diol  
dehydrogenase gene involved in the degradation of gamma-  
hexachlorocyclohexane in Pseudomonas paucimobilis";  
RL J. Bacteriol. 176:3117-3125(1994).  
CC -1- FUNCTION: DEGRADATION OF 2,5-DICHLORO-2,5-CYCLOHEXADIENE-1,4-DIOL  
(2,5-DDOL) INTO 2,5-DICHLOROHYDROQUINONE (2,5-DCHQ). LNK IS NOT  
ESSENTIAL TO GAMMA-HCH DEGRADATION.  
CC -1- PATHWAY: Degradation of gamma-hexachlorocyclohexane.  
CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases  
(SDR) family.  
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CC -----  
DR EMBL; D23722; BAA04939.1; -  
DR HSPSP; P19992; 1HDC.  
DR InterPro; IPR002198; ADH\_short.  
DR Pfam; PF00106; adh\_short; 1.  
DR PRINTS; PR00080; SDRFAMILY.  
DR PROSITE; PS00061; ADH\_SHORT; 1.  
KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.  
FT NP BIND 9 34 NAD (BY SIMILARITY).  
FT ACT SITE 156 156 BY SIMILARITY.  
SQ SEQUENCE 250 AA; 25492 MW; 8C52703FF767382CF CRC64;

Query Match

4.4%; Score 12; DB 1; Length 250;

Best Local Similarity 100.0%; Pred. No. 0.00024;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 13 GKVALITGGASG 24  
Db 7 GKVALITGGASG 18  
RESULT 2  
ID YWFD\_BACSU STANDARD; PRT; 255 AA.  
AC P39640;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Hypothetical oxidoreductase ywfd (EC 1.-.-).  
GN YWFD OR IPA-82D.  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1423;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=168;  
RX MEDLINE=95020537; PubMed=7934828;  
RA Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W.,  
RA Hulio M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer I.,  
RA Presecan G., Santana M., Schneider E., Schweizer J., Vertes A.,  
RA Rapoport G., Danchin A.;  
RT "Bacillus subtilis genome project: cloning and sequencing of the 97  
kb region from 325 degrees to 333 degrees";  
RL Mol. Microbiol. 10:371-384(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=168;  
RX MEDLINE=98044033; PubMed=9384377;  
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
RA Azevedo V., Bextero M.G., Bessieres P., Bolotin A., Borchert S.,  
RA Boriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,  
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,  
RA Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,  
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,  
RA Entian K.D., Errington J., Fabret C., Ferrazi E., Foulger D.,  
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,  
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grand G.,  
RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,  
RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,  
RA Joris B., Karamata D., Kasahara Y., Klaerr-Balchard M., Klein C.,  
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,  
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,  
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,  
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,  
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,  
RA Parro V., Pohl T.M., Portetalle D., Porwollik S., Prescott A.M.,  
RA Presecan G., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,  
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,  
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,  
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,  
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,  
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,  
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,  
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,  
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,  
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;  
RT "The complete genome sequence of the Gram-positive bacterium Bacillus  
subtilis";  
RL Nature 390:249-256(1997).  
CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases  
(SDR) family.  
CC  
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CC -----  
DR EMBL; D23722; BAA04939.1; -  
DR HSPSP; P19992; 1HDC.  
DR InterPro; IPR002198; ADH\_short.  
DR Pfam; PF00106; adh\_short; 1.  
DR PRINTS; PR00080; SDRFAMILY.  
DR PROSITE; PS00061; ADH\_SHORT; 1.  
KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.  
FT NP BIND 9 34 NAD (BY SIMILARITY).  
FT ACT SITE 156 156 BY SIMILARITY.  
SQ SEQUENCE 250 AA; 25492 MW; 8C52703FF767382CF CRC64;

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CC EMBL; X73124; CAA51638.1; -;  
 CC EMBL; Z99123; CAB15799.1; -;  
 CC PIR; S39737; S39737.  
 DR HSSP; P50162; IAE1.  
 DR Subtilisin; BG10628; ywfD.  
 DR InterPro; IPR002198; ADH short.  
 DR Pfam; PF00106; adh\_short\_1.  
 DR PROSITE; PS00080; SDRFAMILY.  
 DR PRINTS; PR00080; SDRFAMILY.  
 KW Hypothetical protein; Oxidoreductase; Complete proteome.  
 FT NP\_BIND 11 33 NAD OR NADP (BY SIMILARITY).  
 FT ACT\_SITE 154 154 BY SIMILARITY.  
 SQ SEQUENCE 255 AA; 27324 MW; 20AA2259BFB8C9B CRC64;

Query Match 3.7%; Score 10; DB 1; Length 255;  
 Best Local Similarity 100.0%; Pred. No. 0.025;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LITGASGIG 26

Db 11 LITGASGIG 20

#### RESULT 3

HC2D\_BOVIN STANDARD; PRT; 261 AA.  
 AC 002691;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH).  
 GN HADH2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=97214648; PubMed=9061028;  
 RA Furuta S., Kobayashi A., Miyazawa S., Hashimoto T.;  
 RT "Cloning and expression of cDNA for a newly identified isozyme of  
 RT bovine liver 3-hydroxyacyl-CoA dehydrogenase and its import into  
 RT mitochondria.";  
 RL Biochim. Biophys. Acta 1350:317-324(1997).  
 CC -1- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA  
 CC + NADH.  
 CC -1- SUBUNIT: Homotetramer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.  
 CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases  
 CC (SDR) family.

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CC EMBL; AB002156; BAAL19510.1; -;  
 CC HSSP; O70351; 1B6W.  
 DR InterPro; IPR002198; ADH short.  
 DR Pfam; PF00106; adh\_short\_1.  
 DR PRINTS; PR00080; SDRFAMILY.  
 DR PROSITE; PS00061; ADH\_SHORT; 1.  
 KW Oxidoreductase; NAD; Mitochondrion.  
 FT NP\_BIND 12 37 NAD (BY SIMILARITY).

FT ACT\_SITE 168 168 BY SIMILARITY.  
 SQ SEQUENCE 261 AA; 27140 MW; 8C7572BGA9A49780 CRC64;

Query Match 3.7%; Score 10; DB 1; Length 261;  
 Best Local Similarity 100.0%; Pred. No. 0.026;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 VALITGASG 24

Db 12 VALITGASG 21

#### RESULT 4

BPHE\_COMTE STANDARD; PRT; 281 AA.  
 AC Q463B1; Q46376;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE C1s-2,3-dihydrobiphenyl-2,3-diol dehydrogenase (EC 1.3.1.56)  
 DE (Biphenyl-2,3-dihydro-2,3-diol dehydrogenase) (2,3-dihydro-2,3-  
 DE dihydroxybiphenyl dehydrogenase) (Biphenyl-cis-diol dehydrogenase)  
 DE (2,3-dihydroxy-4-phenylhexa-4,6-diene dehydrogenase) (B2,3D).  
 GN BPHE.  
 OS Comamonas testosteroni (Pseudomonas testosteroni).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Comamonadaceae; Comamonas.  
 OX NCBI\_TaxID=285;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
 RC STRAIN=B-356;  
 RX MEDLINE=96316386; PubMed=8702262;  
 RA Sylvestre M., Hurtubise Y., Barriault D., Bergeron J., Ahmad D.,  
 RT "Characterization of active recombinant 2,3-dihydro-2,3-  
 RT dihydroxybiphenyl dehydrogenase from Comamonas testosteroni B-356 and  
 RT sequence of the encoding gene (bphB).";  
 RL Appl. Environ. Microbiol. 62:2710-2715(1996).  
 RN [2]  
 RP SEQUENCE OF 1-15 FROM N.A.  
 RC STRAIN=B-356;  
 RX MEDLINE=97045812; PubMed=8890734;  
 RA Sylvestre M., Sirois M., Hurtubise Y., Bergeron J., Ahmad D.,  
 RA Shareck F., Barriault D., Guillemette I., Juteau J.M.;  
 RT "Sequencing of Comamonas testosteroni strain B-356-  
 RT biphenyl/chlorobiphenyl dioxygenase genes: evolutionary relationships  
 RT among Gram-negative bacterial biphenyl dioxygenases.";  
 RL Gene 174:195-202(1996).  
 CC -1- CATALYTIC ACTIVITY: Cis-3-phenylcyclohexa-3,5-diene-1,2-diol +  
 CC NAD(+) = biphenyl-2,3-diol + NADH.  
 CC -1- PATHWAY: DEGRADATION OF BIPHENYLS AND POLYCHLOROBIPHENYLS (PCB) TO  
 CC BENZOIC ACID AND CHLOROBENZOIC ACIDS; SECOND STEP.  
 CC -1- SUBUNIT: Homotetramer.  
 CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases  
 CC (SDR) family.

-----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; U57451; AAB18304.1; -;  
 CC EMBL; U47637; AAC44530.1; -;  
 CC PIR; PC4213; PC4213.  
 DR HSSP; P47227; 1BDB.  
 DR InterPro; IPR002198; ADH short.  
 DR Pfam; PF00106; adh\_short\_1.  
 DR PRINTS; PR00080; SDRFAMILY.  
 DR PROSITE; PS00061; ADH\_SHORT; 1.  
 KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.  
 FT NP\_BIND 10 34 NAD (BY SIMILARITY).

```

FT ACT SITE 155 155 BY SIMILARITY.
SQ SEQUENCE 281 AA; 29350 MW; D50A4CC9167A113E CRC64;

Query Match 3.7%; Score 10; DB 1; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 VALITGGAGS 24
Db 7 VALITGGAGS 16

RESULT 5
GS39_BACSU STANDARD; PRT; 285 AA.
ID _GS39_BACSU STANDARD; PRT; 285 AA.
AC P80873; P96577;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE General stress protein 39 (GSP39) (EC 1.1.1.1).
GN YPAD.
OS Bacillus subtilis.
OC Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]_TaxID=1423;
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kasahara Y., Nakai S., Lee S., Sadaie Y., Ogasawara N.;
RT "A 148 kbp sequence of the region between 35 and 47 degree of the
RL Bacillus subtilis genome.";
RN Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
AZavedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
BRoriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
BRouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
CHoi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
DENIZOT F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
ENTIAN K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
FRITZ C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
GHIM S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
GUISeppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
HILBERT H., Hollappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
JAZIS B., Karanats D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
KOBAYASHI Y., Koester P., Koningsstein G., Krogh S., Kumano M.,
KURITS K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
LEE S.M., Levine A., Liu H., Masuda S., Mavel C., Medigue C.,
MEDINA N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
NOONE D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
PARRO V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
PRESECAN E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RIEGER M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
SATO T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
SEKIGUCHI J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
SOKKIN A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
TAKEUCHI M., Tamakoshi A., Tanaka T., Terpetra P., Tognoni A.,
TOSATO V., Uchiyama S., Vandenbol M., Vannier P., Vassarotti A.,
VIARI A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
WINTERS P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
YOSHIDA K., Yoshikawa H.P., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
subtilis.";
RL Nature 390:249-256 (1997).
[3]
RP SEQUENCE OF 1-29.
RC STRAIN=168 / 1S58;
RX MEDLINE=97443988; PubMed=9298659;
RA Artelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
HECKER M.;
RT "First steps from a two-dimensional protein index towards a response-
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regulation map for Bacillus subtilis.";
RL Electrophoresis 18:1451-1463 (1997).
CC -I- INDUCTION: BY HEAT SHOCK, SALT STRESS, OXIDATIVE STRESS, GLUCOSE
LIMITATION AND OXYGEN LIMITATION.
CC -I- SIMILARITY: belongs to the short-chain dehydrogenases/reductases
(SDR) family.
CC -----
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CC -----
EMBL; AB001488; BAA19257.1; -.
DR EMBL; Z99106; CAB12226.1; -.
DR PIR; D69768; D69768.
DR HSP; P50162; 1AE1.
DR Subtilisin; BG12052; ydad.
DR InterPro; IPR002198; ADH short.
PFam; PF00106; adh short; 1.
PRINTS; P00080; SDRFAMILY.
PROSITE; PS00061; ADH SHORT; 1.
KW Oxidoreductase; Heat shock; Complete proteome.
FT INIT MET 0
FT NP BIND 45 69 NAD OR NADP (BY SIMILARITY).
FT ACT SITE 190 190 BY SIMILARITY.
FT CONFLICT 21 21 E -> G (IN REF. 3).
FT CONFLICT 26 26 P -> K (IN REF. 3).
SQ SEQUENCE 285 AA; 30951 MW; 98A7EF096B2C9AAE CRC64;

Query Match 3.3%; Score 9; DB 1; Length 285;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 GKVALITGG 21
Db 41 GKVALITGG 49

RESULT 6
YUXG_BACSU STANDARD; PRT; 689 AA.
ID YUXG_BACSU STANDARD; PRT; 689 AA.
AC P40747;
DT 01-FEB-1995 (Rel. 31, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical oxidoreductase yuxG (EC 1.1.1.1) (ORF2).
YUXG OR YULA.
GN Bacillus subtilis.
OC Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=97419515; PubMed=9274030;
RA Oudega B., Koningsstein G., Rodrigues L., de Sales Ramon M.,
HILBERT H., Dusterhoft A., Pohl T.M., Weitzenecker T.;
RT "Analysis of the Bacillus subtilis genome: cloning and nucleotide
sequence of a 62 kb region between 275 degrees (trnB) and 284 degrees
(pai).";
RL Microbiology 143:2769-2774 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
AZavedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
BRoriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
BRouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
CHoi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
DENIZOT F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
ENTIAN K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
FRITZ C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
GHIM S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
GUISeppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
HILBERT H., Hollappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
JAZIS B., Karanats D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
KOBAYASHI Y., Koester P., Koningsstein G., Krogh S., Kumano M.,
KURITS K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
LEE S.M., Levine A., Liu H., Masuda S., Mavel C., Medigue C.,
MEDINA N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
NOONE D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
PARRO V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
PRESECAN E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RIEGER M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
SATO T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
SEKIGUCHI J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
SOKKIN A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
TAKEUCHI M., Tamakoshi A., Tanaka T., Terpetra P., Tognoni A.,
TOSATO V., Uchiyama S., Vandenbol M., Vannier P., Vassarotti A.,
VIARI A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
WINTERS P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
YOSHIDA K., Yoshikawa H.P., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
subtilis.";
RL Nature 390:249-256 (1997).
[3]
RP SEQUENCE OF 1-29.
RC STRAIN=168 / 1S58;
RX MEDLINE=97443988; PubMed=9298659;
RA Artelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
HECKER M.;
RT "First steps from a two-dimensional protein index towards a response-
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RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Paro V., Pohl T.M., Portetelle D., Rapoport G., Rey M., Reynolds S.,
RA Prescan E., Pujic P., Purnelle B., Rappoport G., Rose M., Sadale Y.,
RA Rieger M., Rivolta C., Roche B., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terpsira P., Tognoni A.,
RA Tobato V., Uchiyama S., Vandenbol M., Vannier P., Vassarotti A.,
RA Viari A., Wambuit R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
RA "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256 (1997).
RN [3]
RP SEQUENCE OF 1-49 FROM N.A.
RX STRAIN=168 / O11085;
RX MEDLINE=94245722; PubMed=8188684;
RA Haulon D.W., Ordal G.W.;
RT "Cloning and characterization of genes encoding methyl-accepting
RT chemotaxis proteins in Bacillus subtilis.";
RL J. Biol. Chem. 269:14038-14046 (1994).
CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC -----
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CC -----
DR EMBL; Z93938; CAB07952.1; -;
DR EMBL; Z99119; CAB15100.1; -;
DR EMBL; Z99120; CAB15111.1; -;
DR EMBL; L29189; AAA20558.2; -;
DR PIR; H70024; H70024.
DR HSSP; P25529; 1FMC.
DR Subtilisin; BG10947; YuxG.
DR InterPro; IPR002198; ADH short.
DR Pfam; PF00106; adh_short; 1.
DR PROSITE; PS00061; Aldolase II; 1.
DR Hypothetical protein; Oxidoreductase; Complete proteome.
FT ACT_SITE 579 579 BY SIMILARITY.
SQ SEQUENCE 689 AA; 76020 MW; 8BA82FDC3EEDD0FD CRC64;

Query Match 3.3%; Score 9; DB 1; Length 689;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 KVALITGA 22
Db 428 KVALITGA 436

RESULT 7
KDUJ_ERWCH
ID_KDUJ_ERWCH STANDARD; PRT; 253 AA.
AC Q05528;
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DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 2-deoxy-D-glucuronate 3-dehydrogenase (EC 1.1.1.125) (2-keto-3-
DE deoxyglucuronate oxidoreductase).
GN KDUJ.
OS Erwinia chrysanthemi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=556;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=3937;
RX MEDLINE=92114798; PubMed=1766386;
RA Condemine G., Robert-Baudouy J.;
RT "Analysis of an Erwinia chrysanthemi gene cluster involved in pectin
RT degradation.";
RL Mol. Microbiol. 5:2191-2202 (1991).
CC -!- CATALYTIC ACTIVITY: 2-deoxy-D-glucuronate + NAD(+) = 3-dehydro-2-
CC deoxy-D-glucuronate + NADH.
CC -!- PATHWAY: Pectin degradation.
CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
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CC -----
DR EMBL; X62073; CAA43989.1; -;
DR PIR; S17711; S17711.
DR HSSP; P19992; IHDC.
DR InterPro; IPR002198; ADH short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase; NAD.
FT NP_BIND 14 38 NAD (BY SIMILARITY).
FT ACT_SITE 158 158 BY SIMILARITY.
SQ SEQUENCE 253 AA; 27275 MW; 59E9827DEA471F76 CRC64;

Query Match 2.9%; Score 8; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 GKVALITG 20
Db 10 GKVALITG 17

RESULT 8
SORD_KLEPN
ID_SORD_KLEPN STANDARD; PRT; 267 AA.
AC P37079;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Sorbitol-6-phosphate 2-dehydrogenase (EC 1.1.1.140) (Glucitol-6-
DE phosphate dehydrogenase) (Ketosephosphate reductase).
GN SORD.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=1033-SP14 / KAY2026;
RX MEDLINE=95035038; PubMed=7947968;
RA Wehmeier U.F., Lengeler J.W.;
RT "Sequence of the sor-operon for L-sorbose utilization from Klebsiella
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RT pneumoniae KAY2026. ";
RL Biochim. Biophys. Acta 1208:348-351 (1994).
RN [2]
RP MEDLINE=95380679; PubMed=7652212;
RA Raizer J., Reizer A., Saier M.H. Jr.;
RT "sorbose-1-P reductase (SOR) and the glucitol-6-P dehydrogenase
RT (SORD) of the Klebsiella pneumoniae L-sorbose operon belong to the
RT zinc-dependent dehydrogenase family and the short chain alcohol
RT dehydrogenase family, respectively.";
RL Res. Microbiol. 146:183-184 (1995).
CC -1- CATALYTIC ACTIVITY: D-sorbitol 6-phosphate + NAD(+) = D-fructose
CC 6-phosphate + NADH.
CC -1- PATHWAY: SORBITOL METABOLIC PATHWAY.
CC -1- SUBUNIT: Homotetramer (By similarity).
CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC
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CC -----
DR EMBL; X66059; CA646856.1; -.
DR F1R; S50186; S50186.
DR HSP; F50162; IAE1.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase; NAD.
FT NP BIND 9 38 NAD (BY SIMILARITY).
FT ACT SITE 160 160 BY SIMILARITY.
SQ SEQUENCE 267 AA; 29005 MW; 44A9C31964384DEC CRC64;

Query Match 2.9%; Score 8; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 TGGAGGIG 26
Db 15 TGGAGGIG 22

RESULT 9
BPHB_PSEPS STANDARD; PRT; 275 AA.
AC P08694;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C1s-2,3-dihydroxybiphenyl-2,3-diol dehydrogenase (EC 1.3.1.56)
DE (Biphenyl-1,2,3-dihydro-2,3-diol dehydrogenase) (2,3-dihydro-2,3-
DE dihydroxybiphenyl dehydrogenase) (Biphenyl-cis-diol dehydrogenase)
DE (2,3-dihydroxy-4-phenylhexa-4,6-diene dehydrogenase).
DN BPHB.
OS Pseudomonas pseudoalcaligenes.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=330;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KF707;
RX MEDLINE=87083404; PubMed=3793719;
RA Furukawa K., Aizawa N., Miyazaki T.;
RT "Nucleotide sequence of the 2,3-dihydroxybiphenyl dioxygenase gene of
RT Pseudomonas pseudoalcaligenes.";
RL J. Bacteriol. 169:427-429 (1987).
CC -1- CATALYTIC ACTIVITY: C1s-3-phenylcyclohexa-3,5-diene-1,2-diol +
CC NAD(+) = biphenyl-2,3-diol + NADH.

```

```

CC -1- PATHWAY: DEGRADATION OF BIPHENYLS AND POLYCHLOROBIPHENYLS (PCB) TO
CC BENZOIC ACID AND CHLOROBENZOIC ACIDS; SECOND STEP.
CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M15333; AAA25752.1; ALT_INIT.
DR HSP; P47227; IBD8.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.
FT NP BIND 9 33 NAD (BY SIMILARITY).
FT ACT SITE 153 153 BY SIMILARITY.
SQ SEQUENCE 275 AA; 28726 MW; F32A4A870B47E566 CRC64;

Query Match 2.9%; Score 8; DB 1; Length 275;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LITGGASG 24
Db 9 LITGGASG 16

RESULT 10
BPHB_BURCE STANDARD; PRT; 277 AA.
ID BPHB_BURCE
AC P47227;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C1s-2,3-dihydrobiphenyl-2,3-diol dehydrogenase (EC 1.3.1.56)
DE (Biphenyl-1,2,3-dihydro-2,3-diol dehydrogenase) (2,3-dihydro-2,3-
DE dihydroxybiphenyl dehydrogenase) (Biphenyl-cis-diol dehydrogenase)
DE (2,3-dihydroxy-4-phenylhexa-4,6-diene dehydrogenase).
DN BPHB.
OS Burkholderia cepacia (Pseudomonas cepacia).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LB400;
RX MEDLINE=93345822; PubMed=8344527;
RA Hofer B., Eltis L.D., Dowling D.N., Timmis K.N.;
RT "Genetic analysis of a Pseudomonas locus encoding a pathway for
RT biphenyl/polychlorinated biphenyl degradation.";
RL Gene 130:47-55 (1993).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=98318037; PubMed=9655331;
RA Huelsmeyer M., Hecht H.-J., Niefind K., Hofer B., Eltis L.D.,
RA Timmis K.N., Schomburg D.;
RT "Crystal structure of cis-biphenyl-2,3-dihydrodiol-2,3-dehydrogenase
RT from a PCB degrader at 2.0-A resolution.";
RL Protein Sci. 7:1286-1293 (1998).
CC -1- CATALYTIC ACTIVITY: C1s-3-phenylcyclohexa-3,5-diene-1,2-diol +
CC NAD(+) = biphenyl-2,3-diol + NADH.
CC -1- PATHWAY: DEGRADATION OF BIPHENYLS AND POLYCHLOROBIPHENYLS (PCB) TO
CC BENZOIC ACID AND CHLOROBENZOIC ACIDS; SECOND STEP.
CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC
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-----

DR EMBL; X66122; CAA46909.1; -;  
DR PIR; JN0814; JN0814.  
DR PDB; 1BD8; 12-NOV-97.  
DR InterPro; IPR002198; ADH short.  
DR Pfam; PF00106; adh\_short; 1.  
DR PRINTS; PR00080; SDRFAMILY.  
DR PROSITE; PS00061; ADH\_SHORT; 1.  
KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD; 3D-structure.  
FT NP\_BIND 9 33 NAD (BY SIMILARITY).  
FT ACT\_SITE 155 155 BY SIMILARITY.  
FT TURN 2 5  
FT STRAND 7 11  
FT TURN 12 14  
FT HELIX 16 27  
FT TURN 28 29  
FT STRAND 31 36  
FT HELIX 39 49  
FT HELIX 50 52  
FT STRAND 53 57  
FT TURN 60 61  
FT HELIX 63 77  
FT STRAND 82 84  
FT TURN 92 93  
FT HELIX 96 98  
FT TURN 101 103  
FT HELIX 104 115  
FT TURN 116 116  
FT HELIX 117 133  
FT TURN 134 134  
FT STRAND 136 140  
FT HELIX 143 145  
FT TURN 146 146  
FT TURN 148 149  
FT HELIX 153 173  
FT TURN 174 176  
FT STRAND 178 184  
FT HELIX 195 197  
FT HELIX 209 213  
FT TURN 214 216  
FT TURN 218 219  
FT HELIX 225 228  
FT HELIX 230 236  
FT HELIX 238 241  
FT TURN 242 243  
FT STRAND 248 251  
FT HELIX 255 257  
FT TURN 267 268  
FT HELIX 269 273  
FT TURN 274 274  
SQ SEQUENCE 277 AA; 28901 MW; 00194120BD4E12D1 CRC64;

Query Match 2.9%; Score 8; DB 1; Length 277;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LITGASG 24  
| | | | |  
Db 9 LITGASG 16

RESULT 11  
BPHB PSEPU  
ID BPHB PSEPU STANDARD; PRT; 277 AA.  
AC P72220;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Cis-2,3-dihydrobiphenyl-2,3-diol dehydrogenase (EC 1.3.1.56)  
DE (Biphenyl-2,3-dihydro-2,3-diol dehydrogenase) (2,3-dihydro-2,3-  
DE dihydroxybiphenyl dehydrogenase) (Biphenyl-cis-diol dehydrogenase)  
DE (2,3-dihydroxy-4-phenylhexa-4,6-diene dehydrogenase).  
GN BPHB.  
OS Pseudomonas putida.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=303;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=OUB3;  
RX MEDLINE=97457193; PubMed=9311131;  
RA Khan A.A., Wang R.F., Nawaz M.S., Cerniglia C.E.;  
RT "Nucleotide sequence of the gene encoding cis-biphenyl dihydrodiol  
RT dehydrogenase (bphB) and the expression of an active recombinant His-  
RT tagged bphB gene product from a PCB degrading bacterium, Pseudomonas  
RT putida OUB3.";  
RL FEMS Microbiol. Lett. 154:317-324(1997).  
CC -1- CATALYTIC ACTIVITY: Cis-3-phenylcyclohexa-3,5-diene-1,2-diol +  
CC NAD(+) = biphenyl-2,3-diol + NADH.  
CC -1- PATHWAY: DEGRADATION OF BIPHENYLS AND POLYCHLOROBIPHENYLS (PCB) TO  
CC BENZOIC ACID AND CHLOROGENOIC ACIDS; SECOND STEP.  
CC -1- SUBUNIT: Homotetramer (Probable).  
CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases  
CC (SDR) family.  
-----  
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-----  
CC EMBL; Y07655; CAA68939.1; -;  
DR HSPSP; P47227; 1BD8.  
DR InterPro; IPR002198; ADH short.  
DR Pfam; PF00106; adh\_short; 1.  
DR PRINTS; PR00080; SDRFAMILY.  
DR PROSITE; PS00061; ADH\_SHORT; 1.  
KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.  
FT NP\_BIND 9 33 NAD (BY SIMILARITY).  
FT ACT\_SITE 155 155 BY SIMILARITY.  
SQ SEQUENCE 277 AA; 28907 MW; A7048159903BE527 CRC64;  
Query Match 2.9%; Score 8; DB 1; Length 277;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 17 LITGASG 24  
| | | | |  
Db 9 LITGASG 16  
RESULT 12  
GSHR BURCE STANDARD; PRT; 449 AA.  
AC P48639;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Glutathione reductase (EC 1.6.1.7) (GR) (Grase).  
GN GOR.  
OS Burkholderia cepacia (Pseudomonas cepacia).  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Burkholderiaceae; Burkholderia.  
OX NCBI\_TaxID=292;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AC1100;  
RX MEDLINE=95266809; PubMed=7538273;

RA Daubaras D.L., Hershberger C.D., Kitano K., Chakrabarty A.M.;  
 RT "sequence analysis of a gene cluster involved in metabolism of 2,4,5-  
 RL trichlorophenoxyacetic acid by Burkholderia cepacia AC100.";  
 CC Appl. Environ. Microbiol. 61:1279-1289(1995).  
 CC -1- CATALYTIC ACTIVITY: 2 glutathione + NADP(+) = glutathione  
 CC disulfide + NADPH.  
 CC -1- COFACTOR: FAD.  
 CC -1- PATHWAY: 2,4,5-trichlorophenoxyacetic acid degradation.  
 CC -1- SUBUNIT: Homodimer (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- MISCELLANEOUS: THE ACTIVE SITE IS A REDOX-ACTIVE DISULFIDE BOND.  
 CC -1- SIMILARITY: BELONGS TO THE PYRIDINE NUCLEOTIDE-DISULFIDE  
 CC OXIDOREDUCTASES CLASS-I.  
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 CC -----  
 CC EMBL: U19883; AAC43334.1; -;  
 CC PIR: I40178; I40178.  
 CC HSP: P28593; IAOG.  
 CC InterPro: IPR001327; FAD\_Pyr\_redox.  
 CC InterPro: IPR006324; Glut\_reduct\_2.  
 CC InterPro: IPR000815; Hg\_reductase.  
 CC InterPro: IPR001100; Pyr\_redox.  
 CC InterPro: IPR004039; Pyr\_redox\_dlm.  
 CC Pfam: PF00070; Pyr\_redox; 1.  
 CC Pfam: PF02852; Pyr\_redox\_dlm; 1.  
 CC PRINTS: PR00368; FADPNR.  
 CC PRINTS: PR00945; HGRDTASE.  
 CC PRINTS: PR00411; PNDRTASEI.  
 CC PRODOM: PD000139; FAD\_Pyr\_redox; 1.  
 CC TIGR: TIGR01424; Gluta\_reduc\_2; 1.  
 CC PROSITE: PS00076; PYRIDINE\_REDOX\_1; 1.  
 CC Redox-active center; Oxidoreductase; Flavoprotein; FAD; NADP.  
 CC NP\_BIND 7 37 FAD (ADP PART) (PROBABLE).  
 CC DLSULFID 43 48 REDOX-ACTIVE (BY SIMILARITY).  
 CC NP\_BIND 292 302 FAD (FLAVIN PART) (BY SIMILARITY).  
 CC ACT\_SITE 435 435 BY SIMILARITY.  
 CC ACT\_SITE 449 AA; 47541 MW; 402FCG6E7A8D6720 CRC64;  
 CC SEQUENCE 449 AA; 2.9%; Score 8; DB 1; Length 449;  
 CC Query Match 2.9%; Score 8; DB 1; Length 449;  
 CC Best Local Similarity 100.0%; Pred. No. 4.4; Indels 0; Gaps 0;  
 CC Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 36 HGAKVAIA 43  
 Db 27 HGAKVAIA 34  
 RESULT 13  
 ID R27A SCHPO STANDARD; PRT; 136 AA.  
 AC O14388; O74167;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE 60S Ribosomal protein L27-A.  
 GN RPL27A OR SPAC695.07C  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 CC Schizosaccharomycetes; Schizosaccharomycetaceae;  
 CC Schizosaccharomycetes.  
 CC NBI\_TaxID=4896;  
 CC [1]  
 RN RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=21848401; PubMed=11859360;  
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Sgouros J., Peat N., Hayles J., Baker S., Bigham D., Bowman S.,  
 RA Brooks K., Brown D., Brown S., Chillingworth T., Church C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagals K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeil C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skellern J., Simmonds M., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,  
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Wedler H., Mambou R., Purnelle B.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloub S., Lelaure V., Mottier S.,  
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucas M., Rechet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;  
 RT "The genome sequence of Schizosaccharomyces pombe.";  
 RL Nature 415:871-880(2002).  
 RN [2]  
 CC SEQUENCE OF 1-74 FROM N.A.  
 RC STRAIN=972;  
 RA Jang Y.J., Yoo H.S.;  
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 CC SEQUENCE OF 4-136 FROM N.A.  
 RT Kawamukai M.;  
 RA "S.pombe ribosomal protein L27 homolog.";  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- MISCELLANEOUS: THERE ARE TWO GENES FOR L27 IN S.POMBE.  
 CC -1- SIMILARITY: BELONGS TO THE L27E FAMILY OF RIBOSOMAL PROTEINS.  
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 CC -----  
 CC EMBL: AL049474; CAB39364.1; -;  
 CC EMBL: U97385; AAB53877.1; -;  
 CC EMBL: AB015354; BAA28649.1; -;  
 CC PIR: T40638; T40638.  
 CC PIR: T43374; T43374.  
 CC GeneDB Spombe; SPBC685.07c; -;  
 CC InterPro: IPR005824; KOW.  
 CC InterPro: IPR006646; KOW sub.  
 CC InterPro: IPR001141; Ribosomal\_L27e.  
 CC Pfam: PF00467; KOW; 1.  
 CC Pfam: PF01777; Ribosomal\_L27e; 1.  
 CC ProDom: PD009396; Ribosomal\_L27e; 1.  
 CC SMART: SM00739; KOW; 1.  
 CC PROSITE: PS01107; RIBOSOMAL\_L27e; 1.  
 CC Ribosomal protein, Multigene family.  
 CC CONFLICT 4 6 ILK -> GTR (IN REF. 3).  
 CC SEQUENCE 136 AA; 15389 MW; 3D5C1526AD501F72 CRC64;  
 CC Query Match 2.6%; Score 7; DB 1; Length 136;  
 CC Best Local Similarity 100.0%; Pred. No. 16;  
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 13 GKVALIT 19  
 Db 8 GKVALIT 14

```
RESULT 14
GLB2_ASCSU          STANDARD;          PRT;   153 AA.
AC P49672;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Myoglobin (Globin, body wall isoform).
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Body wall muscle;
RA MEDLINE=95074010; PubMed=7982924;
RX Blaxter M.L., Vanfleteren J.R., Xia J., Moens L.;
RT "Structural characterization of an Ascaris myoglobin.";
RL J. Biol. Chem. 269:30181-30186(1994).
CC -!- FUNCTION: HIGH OXYGEN AFFINITY. PROBABLY SUPPLIES OXYGEN NEEDED
CC FOR MUSCLE ACTIVITY.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: BODY WALL GLOBIN IS LOCALIZED IN CELLULAR
CC COMPARTMENTS BELONGING TO THE HYPODERMIS, THE DORSAL, VENTRAL AND
CC LATERAL CORDS, THE NERVE RING, AND BODY WALL MUSCLE.
CC -!- PTM: THE N-TERMINUS IS BLOCKED.
CC -!- SIMILARITY: Belongs to the globin family.
CC -----
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CC -----
DR EMBL; U17337; AAA64695.1; -.
DR PIR; A55139; A55139.
DR HSSP; P28316; 1ASH.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; Globin; 1.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport.
FT METAL 94
FT IRON (HEME PROXIMAL LIGAND)
FT (BY SIMILARITY)
SQ SEQUENCE 153 AA; 17454 MW; 1B3EF94A15B49B98 CRC64;

Query Match          2.6%; Score 7; DB 1; Length 153;
Best Local Similarity 100.0%; Pred.No.18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 198 ALGKKFS 204
    |||||
Db 133 ALGKKFS 139

RESULT 15
Q5B_CAEEL
ID -Q5B_CAEEL          STANDARD;          PRT;   154 AA.
AC Q09254;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical 15.4 kDa protein C16C10.11 in chromosome III.
GN C16C10.11.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
```

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RA Lloyd C.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; Z46787; CAA86749.1; -.
DR PIR; T19332; T19332.
DR WormPep; C16C10.11; CE01491.
DR InterPro; IPR007017; DUF657.
DR Pfam; PF04933; DUF657; 1.
KW Hypothetical protein.
SQ SEQUENCE 154 AA; 15388 MW; 5F5C618B637D2683 CRC64;

Query Match          2.6%; Score 7; DB 1; Length 154;
Best Local Similarity 100.0%; Pred.No.18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 155 GGGSSHA 161
    |||||
Db 90 GGGSSHA 96

Search completed: October 23, 2003, 13:03:11
Job time : 55 secs
```



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OM protein - protein search, using sw model

Run on: October 23, 2003, 12:59:05 ; Search time 96 Seconds  
(without alignments)  
733.837 Million cell updates

Title: US-09-673-918A-2  
Perfect score: 273  
Sequence: 1 MQLTAFARRLEGKVALITG.....IDGGFVCNSVIKVFQYPS 273

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : SPTREMBL 23:\*

- ```

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvrvs:*
16: sp_bacteriap:*
17: sp_archeap:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query |     | Length | DB     | ID     | Description. |
|------------|-------|-------|-----|--------|--------|--------|--------------|
|            |       | Match | %   |        |        |        |              |
| 1          | 110   | 40.3  | 277 | 10     | Q94KL7 | Q94KL7 | forssythia i |
| 2          | 17    | 6.2   | 234 | 10     | Q40590 | Q40590 | nicotiana t  |
| 3          | 17    | 6.2   | 284 | 10     | O50038 | O50038 | nicotiana t  |
| 4          | 16    | 5.9   | 283 | 10     | Q9ZRL7 | Q9ZRL7 | arabidopsis  |
| 5          | 14    | 5.1   | 306 | 10     | Q941B4 | Q941B4 | arabidopsis  |
| 6          | 14    | 5.1   | 306 | 10     | Q9LW34 | Q9LW34 | arabidopsis  |
| 7          | 13    | 4.8   | 267 | 10     | P93697 | P93697 | vigna ungu   |
| 8          | 13    | 4.8   | 274 | 10     | Q8H0D9 | Q8H0D9 | phaseolus l  |
| 9          | 13    | 4.8   | 321 | 10     | O8L1D4 | O8L1D4 | oryza sativ  |
| 10         | 12    | 4.4   | 160 | 10     | Q8S9B7 | Q8S9B7 | ipomoea tri  |
| 11         | 12    | 4.4   | 277 | 10     | Q9SBD7 | Q9SBD7 | ipomoea tri  |
| 12         | 12    | 4.4   | 277 | 10     | Q9SBD8 | Q9SBD8 | ipomoea tri  |
| 13         | 12    | 4.4   | 284 | 10     | Q9SBD6 | Q9SBD6 | ipomoea tri  |
| 14         | 12    | 4.4   | 284 | 10     | O82465 | O82465 | ipomoea tri  |
| 15         | 11    | 4.0   | 278 | 3      | P87017 | P87017 | aspergillus  |
| 16         | 11    | 4.0   | 278 | 3      | Q8J2U8 | Q8J2U8 | aspergillus  |

|     |   |     |     |    |         |                     |     |   |     |     |    |         |                     |
|-----|---|-----|-----|----|---------|---------------------|-----|---|-----|-----|----|---------|---------------------|
| 90  | 8 | 2.9 | 263 | 16 | Q9RJY4  | Q9TJ4 streptomyce   | 163 | 7 | 2.6 | 250 | 2  | Q8GDE6  | Q8gde6 pseudomonas  |
| 91  | 8 | 2.9 | 268 | 10 | Q9SOF9  | Q9af9 pium sativ    | 164 | 7 | 2.6 | 251 | 2  | Q9F7E0  | Q9f7e0 acinetobact  |
| 92  | 8 | 2.9 | 268 | 10 | Q9SQJ3  | Q9sqj3 pium sativ   | 165 | 7 | 2.6 | 251 | 5  | Q9VS71  | Q9vs71 drosophila   |
| 93  | 8 | 2.9 | 268 | 16 | Q8X5Z2  | Q8x5z2 escherichia  | 166 | 7 | 2.6 | 251 | 10 | Q40133  | Q40133 lycopersico  |
| 94  | 8 | 2.9 | 268 | 16 | Q8FP84  | Q8fb49 escherichia  | 167 | 7 | 2.6 | 251 | 15 | Q8PR00  | Q8pr00 xanthomonas  |
| 95  | 8 | 2.9 | 271 | 2  | Q23236  | Q22316 clostridium  | 168 | 7 | 2.6 | 251 | 16 | Q8PE31  | Q8pe31 xanthomonas  |
| 96  | 8 | 2.9 | 272 | 2  | Q9LC88  | Q9l588 nocardioide  | 169 | 7 | 2.6 | 252 | 4  | Q56HD5  | Q56hd5 homo sapien  |
| 97  | 8 | 2.9 | 276 | 2  | Q9L748  | Q9l748 pseudomonas  | 170 | 7 | 2.6 | 252 | 15 | Q8CQ73  | Q8cq73 staphylococ  |
| 98  | 8 | 2.9 | 276 | 2  | Q9S570  | Q9s570 pseudomonas  | 171 | 7 | 2.6 | 252 | 17 | Q9YC93  | Q9yc93 aeropyrum p  |
| 99  | 8 | 2.9 | 277 | 2  | Q9AEY1  | Q9aey1 pseudomonas  | 172 | 7 | 2.6 | 253 | 16 | Q8XPA8  | Q8xpa8 clostridium  |
| 100 | 8 | 2.9 | 277 | 2  | Q8S287  | Q8s287 sphingomona  | 173 | 7 | 2.6 | 254 | 16 | Q8EMX3  | Q8emx3 oceanobacil  |
| 101 | 8 | 2.9 | 277 | 2  | Q8S2030 | Q8s2030 pseudomonas | 174 | 7 | 2.6 | 255 | 16 | P95286  | P95286 mycobacteri  |
| 102 | 8 | 2.9 | 278 | 16 | Q9RWY1  | Q9rwy1 deinococcus  | 175 | 7 | 2.6 | 255 | 16 | Q92RW7  | Q92rw7 rhizobium m  |
| 103 | 8 | 2.9 | 279 | 5  | Q9XTD5  | Q9xtd5 caenorhabdi  | 176 | 7 | 2.6 | 255 | 16 | Q92L2C9 | Q92l2c9 streptomyce |
| 104 | 8 | 2.9 | 285 | 16 | Q8YLW4  | Q8ylw4 anabaena sp  | 177 | 7 | 2.6 | 257 | 16 | Q983U4  | Q983u4 rhizobium l  |
| 105 | 8 | 2.9 | 286 | 3  | Q9HE38  | Q9he38 neurospora   | 178 | 7 | 2.6 | 257 | 16 | Q8UBE2  | Q8ube2 agrobacteri  |
| 106 | 8 | 2.9 | 287 | 16 | Q987Y1  | Q987y1 rhizobium l  | 179 | 7 | 2.6 | 258 | 16 | Q8PG10  | Q8pg10 xanthomonas  |
| 107 | 8 | 2.9 | 289 | 16 | Q8CN03  | Q8cn03 staphylococ  | 180 | 7 | 2.6 | 258 | 16 | Q8P4E8  | Q8p4e8 xanthomonas  |
| 108 | 8 | 2.9 | 295 | 2  | P94129  | P94129 acinetobact  | 181 | 7 | 2.6 | 258 | 16 | Q8EN56  | Q8en56 oceanobacil  |
| 109 | 8 | 2.9 | 296 | 16 | Q9ABX6  | Q9abx6 caulobacter  | 182 | 7 | 2.6 | 259 | 10 | Q9LEG3  | Q9leg3 lycopersico  |
| 110 | 8 | 2.9 | 299 | 16 | Q97J63  | Q97j63 clostridium  | 183 | 7 | 2.6 | 259 | 16 | Q98GY6  | Q98gy6 rhizobium l  |
| 111 | 8 | 2.9 | 319 | 10 | Q9SK30  | Q9sk30 arabidopsis  | 184 | 7 | 2.6 | 260 | 16 | Q98H11  | Q98h11 rhizobium l  |
| 112 | 8 | 2.9 | 321 | 10 | Q9LG18  | Q9lg18 oryza sativ  | 185 | 7 | 2.6 | 261 | 16 | Q9PEW5  | Q9pew5 xylella fas  |
| 113 | 8 | 2.9 | 331 | 16 | Q8GGG9  | Q8ggg9 rhizobium l  | 186 | 7 | 2.6 | 261 | 16 | Q9AB11  | Q9ab11 caulobacter  |
| 114 | 8 | 2.9 | 391 | 16 | Q8PGS3  | Q8pgs3 xanthomonas  | 187 | 7 | 2.6 | 261 | 16 | Q8UE56  | Q8ue56 agrobacteri  |
| 115 | 8 | 2.9 | 424 | 16 | Q8F5H1  | Q8feh1 corynebacte  | 188 | 7 | 2.6 | 261 | 16 | Q8UE53  | Q8ue53 agrobacteri  |
| 116 | 8 | 2.9 | 629 | 10 | Q9FX95  | Q9fx95 arabidopsis  | 189 | 7 | 2.6 | 263 | 16 | Q8D564  | Q8d564 yersinia pe  |
| 117 | 8 | 2.9 | 629 | 10 | Q39174  | Q39174 arabidopsis  | 190 | 7 | 2.6 | 263 | 16 | Q8U713  | Q8u713 agrobacteri  |
| 118 | 8 | 2.9 | 657 | 16 | P73359  | P73359 synchococyst | 191 | 7 | 2.6 | 264 | 16 | Q8U713  | Q8u713 agrobacteri  |
| 119 | 8 | 2.9 | 36  | 3  | Q14387  | Q14387 schizosacch  | 192 | 7 | 2.6 | 266 | 16 | Q92BP4  | Q92bp4 rhizobium m  |
| 120 | 7 | 2.6 | 95  | 3  | Q9YH77  | Q9yh77 piromyces s  | 193 | 7 | 2.6 | 267 | 2  | Q9AQN5  | Q9agn5 pseudomonas  |
| 121 | 7 | 2.6 | 107 | 16 | Q8XK08  | Q8xk08 clostridium  | 194 | 7 | 2.6 | 269 | 2  | Q8GI30  | Q8gi30 pseudomonas  |
| 122 | 7 | 2.6 | 111 | 16 | Q8VJS7  | Q8vjs7 mycobacteri  | 195 | 7 | 2.6 | 269 | 2  | Q8GI30  | Q8gi30 pseudomonas  |
| 123 | 7 | 2.6 | 111 | 17 | Q9YD33  | Q9yd33 aeropyrum p  | 196 | 7 | 2.6 | 271 | 16 | Q8U612  | Q8u612 agrobacteri  |
| 124 | 7 | 2.6 | 111 | 17 | Q9F202  | Q9f202 cucumis sat  | 197 | 7 | 2.6 | 274 | 16 | Q8KBL5  | Q8kbl5 chlorobium   |
| 125 | 7 | 2.6 | 118 | 10 | Q8F268  | Q8f268 leptospira   | 198 | 7 | 2.6 | 275 | 16 | Q8E9H5  | Q8eh5 shewanella    |
| 126 | 7 | 2.6 | 132 | 16 | Q8BEG3  | Q8beg3 mus musculu  | 199 | 7 | 2.6 | 281 | 17 | Q29061  | Q29061 archaeoglob  |
| 127 | 7 | 2.6 | 141 | 17 | Q9Y5E1  | Q9ye51 aeropyrum p  | 200 | 7 | 2.6 | 282 | 11 | Q9D3M7  | Q9d3m7 mus musculu  |
| 128 | 7 | 2.6 | 146 | 17 | Q58420  | Q58420 pyrococcus   | 201 | 7 | 2.6 | 282 | 13 | Q73678  | Q73678 oryza lat    |
| 129 | 7 | 2.6 | 159 | 16 | Q9HZ33  | Q9hz33 pseudomonas  | 202 | 7 | 2.6 | 286 | 10 | Q9C7L3  | Q9c7l3 arabidopsis  |
| 130 | 7 | 2.6 | 162 | 2  | Q9L768  | Q9l768 desulfovibr  | 203 | 7 | 2.6 | 286 | 16 | Q9IIX3  | Q9iix3 pseudomonas  |
| 131 | 7 | 2.6 | 165 | 10 | Q8W5E3  | Q8w5e3 oryza sativ  | 204 | 7 | 2.6 | 287 | 10 | Q8LID2  | Q8lid2 oryza sativ  |
| 132 | 7 | 2.6 | 172 | 16 | Q9RT56  | Q9rt56 deinococcus  | 205 | 7 | 2.6 | 289 | 15 | Q9KXK6  | Q9kxk6 streptomyce  |
| 133 | 7 | 2.6 | 181 | 16 | Q9RVH8  | Q9rvh8 deinococcus  | 206 | 7 | 2.6 | 297 | 15 | Q88939  | Q88939 walleye der  |
| 134 | 7 | 2.6 | 183 | 2  | Q9T41   | Q9t41 bacillus an   | 207 | 7 | 2.6 | 298 | 10 | Q9LTV6  | Q9ltv6 arabidopsis  |
| 135 | 7 | 2.6 | 188 | 16 | Q8XEW8  | Q8xew8 salmonella   | 208 | 7 | 2.6 | 300 | 16 | Q8XVI9  | Q8xvi9 ralistonia s |
| 136 | 7 | 2.6 | 190 | 2  | Q9AGH5  | Q9agh5 klebsiella   | 209 | 7 | 2.6 | 306 | 10 | Q8LIC2  | Q8lic2 oryza sativ  |
| 137 | 7 | 2.6 | 191 | 17 | Q29904  | Q29904 archaeoglob  | 210 | 7 | 2.6 | 308 | 16 | Q8XRP5  | Q8xrp5 ralistonia s |
| 138 | 7 | 2.6 | 200 | 10 | Q80711  | Q80711 arabidopsis  | 211 | 7 | 2.6 | 308 | 16 | Q8C9J2  | Q8c9j2 staphylococ  |
| 139 | 7 | 2.6 | 203 | 16 | Q8E028  | Q8e028 streptococc  | 212 | 7 | 2.6 | 315 | 6  | Q95JF5  | Q95jf5 oryctolagus  |
| 140 | 7 | 2.6 | 207 | 5  | Q44951  | Q44951 caenorhabdi  | 213 | 7 | 2.6 | 316 | 10 | Q8LIB9  | Q8lib9 oryza sativ  |
| 141 | 7 | 2.6 | 215 | 3  | Q60171  | Q60171 schizosacch  | 214 | 7 | 2.6 | 316 | 10 | Q8LIB8  | Q8lib8 oryza sativ  |
| 142 | 7 | 2.6 | 217 | 16 | Q917B3  | Q917b3 pseudomonas  | 215 | 7 | 2.6 | 317 | 5  | Q9VRJ4  | Q9vrj4 drosophila   |
| 143 | 7 | 2.6 | 217 | 16 | Q8E5R1  | Q8e5r1 streptococc  | 216 | 7 | 2.6 | 323 | 16 | Q8YLA8  | Q8yla8 anabaena sp  |
| 144 | 7 | 2.6 | 222 | 2  | Q24831  | Q24831 acinetobact  | 217 | 7 | 2.6 | 328 | 16 | Q914J8  | Q914j8 pseudomonas  |
| 145 | 7 | 2.6 | 229 | 2  | Q53064  | Q53064 rhodococcus  | 218 | 7 | 2.6 | 328 | 16 | P72043  | P72043 mycobacteri  |
| 146 | 7 | 2.6 | 231 | 4  | Q07985  | Q07985 homo sapien  | 219 | 7 | 2.6 | 329 | 2  | Q93PV9  | Q93pv9 selenomonas  |
| 147 | 7 | 2.6 | 232 | 16 | Q9PA83  | Q9pa83 xylella fas  | 220 | 7 | 2.6 | 331 | 16 | Q8XH47  | Q8xh47 clostridium  |
| 148 | 7 | 2.6 | 232 | 16 | Q98J95  | Q98j95 rhizobium l  | 221 | 7 | 2.6 | 336 | 2  | Q56866  | Q56866 yersinia en  |
| 149 | 7 | 2.6 | 233 | 12 | Q98RW3  | Q98rw3 guillardia   | 222 | 7 | 2.6 | 339 | 8  | Q36443  | Q36443 mycena galo  |
| 150 | 7 | 2.6 | 233 | 12 | Q91IE2  | Q9lie2 lymantria d  | 223 | 7 | 2.6 | 339 | 16 | Q8Y339  | Q8y339 anabaena sp  |
| 151 | 7 | 2.6 | 239 | 16 | Q8RD37  | Q8rd37 thermoanaer  | 224 | 7 | 2.6 | 340 | 17 | Q8TRK1  | Q8trk1 methanosarc  |
| 152 | 7 | 2.6 | 242 | 2  | Q8AP19  | Q8ap19 methylobact  | 225 | 7 | 2.6 | 346 | 2  | Q9X2W9  | Q9x2w9 rhodospiril  |
| 153 | 7 | 2.6 | 242 | 2  | Q8RG25  | Q8rg25 fusobacteri  | 226 | 7 | 2.6 | 346 | 5  | Q9VE86  | Q9ve86 drosophila   |
| 154 | 7 | 2.6 | 244 | 2  | Q8VLS3  | Q8vls3 xanthobacte  | 227 | 7 | 2.6 | 346 | 5  | Q9VE86  | Q9ve86 drosophila   |
| 155 | 7 | 2.6 | 245 | 16 | Q8YFP3  | Q8yfp3 bruceella me | 228 | 7 | 2.6 | 353 | 16 | Q8XU83  | Q8xu83 ralistonia s |
| 156 | 7 | 2.6 | 245 | 16 | Q8G271  | Q8g271 bruceella su | 229 | 7 | 2.6 | 353 | 16 | Q92N16  | Q92n16 rhizobium m  |
| 157 | 7 | 2.6 | 246 | 16 | Q8ZFW2  | Q8zfw2 yersinia pe  | 230 | 7 | 2.6 | 357 | 5  | Q73770  | Q73770 plasmid me   |
| 158 | 7 | 2.6 | 247 | 2  | Q93RMO  | Q93rmo acinetobact  | 231 | 7 | 2.6 | 362 | 16 | Q9R966  | Q9r966 bruceella me |
| 159 | 7 | 2.6 | 248 | 16 | Q8ZG59  | Q8zgm0 acinetobact  | 232 | 7 | 2.6 | 362 | 16 | Q8G219  | Q8g219 bruceella su |
| 160 | 7 | 2.6 | 248 | 16 | Q8U9R1  | Q8u9r1 yersinia pe  | 233 | 7 | 2.6 | 365 | 3  | Q9HDU4  | Q9hd4 schizosacch   |
| 161 | 7 | 2.6 | 249 | 5  | Q9W4U2  | Q9w4u2 drosophila   | 234 | 7 | 2.6 | 366 | 2  | Q8KJ53  | Q8kj53 rhizobium l  |
| 162 | 7 | 2.6 | 249 | 15 | Q9J6W7  | Q9j6w7 human immu   | 235 | 7 | 2.6 | 366 | 16 | Q98AU5  | Q98au5 rhizobium l  |

|     |   |     |     |    |        |                     |     |   |     |      |    |         |                     |
|-----|---|-----|-----|----|--------|---------------------|-----|---|-----|------|----|---------|---------------------|
| 236 | 7 | 2.6 | 369 | 13 | Q8AV11 | Q8av11 xenopus lae  | 309 | 7 | 2.6 | 824  | 4  | Q8N719  | Q8n719 homo sapien  |
| 237 | 7 | 2.6 | 372 | 2  | Q8VQ49 | Q8vq49 escherichia  | 310 | 7 | 2.6 | 830  | 4  | Q8WVC5  | Q8wvc5 homo sapien  |
| 238 | 7 | 2.6 | 372 | 2  | Q93Q33 | Q93q33 salmonella   | 311 | 7 | 2.6 | 872  | 2  | Q47114  | Q47114 escherichia  |
| 239 | 7 | 2.6 | 372 | 2  | Q9S522 | Q9s522 escherichia  | 312 | 7 | 2.6 | 902  | 5  | O16161  | O16161 mytilus edu  |
| 240 | 7 | 2.6 | 372 | 11 | Q8K0C9 | Q8k0c9 mus musculus | 313 | 7 | 2.6 | 908  | 16 | Q912W3  | Q912w3 pseudomonas  |
| 241 | 7 | 2.6 | 372 | 11 | Q8K3X3 | Q8k3x3 cricetus     | 314 | 7 | 2.6 | 913  | 5  | Q8T3E5  | Q8t3e5 caenorhabdi  |
| 242 | 7 | 2.6 | 372 | 16 | Q8S339 | Q8s339 escherichia  | 315 | 7 | 2.6 | 928  | 2  | Q8RT68  | Q8rt68 bartonella   |
| 243 | 7 | 2.6 | 373 | 16 | Q8Z5H1 | Q8z5h1 salmonella   | 316 | 7 | 2.6 | 928  | 5  | Q19128  | Q19128 caenorhabdi  |
| 244 | 7 | 2.6 | 373 | 16 | Q9F7A4 | Q9f7a4 salmonella   | 317 | 7 | 2.6 | 938  | 11 | Q8BK52  | Q8bk52 mus musculus |
| 245 | 7 | 2.6 | 377 | 2  | Q9LA94 | Q9la94 aeromonas h  | 318 | 7 | 2.6 | 946  | 2  | P70888  | P70888 bacteroides  |
| 246 | 7 | 2.6 | 377 | 10 | Q9M7I6 | Q9m7i6 zea mays (m  | 319 | 7 | 2.6 | 955  | 5  | Q8MQ86  | Q8mq86 caenorhabdi  |
| 247 | 7 | 2.6 | 377 | 17 | Q8Q087 | Q8q087 methanosarc  | 320 | 7 | 2.6 | 960  | 10 | Q8L671  | Q8l671 oryza sativ  |
| 248 | 7 | 2.6 | 377 | 17 | Q8P1P5 | Q8p1p5 methanosarc  | 321 | 7 | 2.6 | 975  | 5  | Q9NK78  | Q9nk78 leishmania   |
| 249 | 7 | 2.6 | 377 | 17 | Q8PW64 | Q8pw64 methanosarc  | 322 | 7 | 2.6 | 1024 | 11 | Q8VDN3  | Q8vdn3 mus musculus |
| 250 | 7 | 2.6 | 377 | 17 | Q8PRR5 | Q8pr5 methanosarc   | 323 | 7 | 2.6 | 1039 | 16 | Q8G4Q1  | Q8g4q1 bifidobacte  |
| 251 | 7 | 2.6 | 380 | 10 | Q94DC9 | Q94dc9 oryza sativ  | 324 | 7 | 2.6 | 1052 | 17 | Q8P2R1  | Q8p2r1 methanosarc  |
| 252 | 7 | 2.6 | 383 | 5  | Q9GZ31 | Q9gz31 trypanosoma  | 325 | 7 | 2.6 | 1088 | 16 | Q8EDG6  | Q8edg6 shewanella   |
| 253 | 7 | 2.6 | 384 | 5  | Q8T8N2 | Q8t8n2 caenorhabdi  | 326 | 7 | 2.6 | 1092 | 16 | Q8EFB4  | Q8efb4 rhizobium l  |
| 254 | 7 | 2.6 | 386 | 4  | Q8WXJ0 | Q8wxj0 homo sapien  | 327 | 7 | 2.6 | 1107 | 3  | Q12271  | Q12271 saccharomyc  |
| 255 | 7 | 2.6 | 390 | 5  | Q9TXJ3 | Q9txj3 leishmania   | 328 | 7 | 2.6 | 1291 | 16 | Q9KU05  | Q9ku05 vibrio chol  |
| 256 | 7 | 2.6 | 395 | 5  | Q8T3U5 | Q8t3u5 halobacteri  | 329 | 7 | 2.6 | 1417 | 10 | Q9FJQ9  | Q9fjg9 arabidopsis  |
| 257 | 7 | 2.6 | 395 | 5  | Q8T3U5 | Q8t3u5 drosophila   | 330 | 7 | 2.6 | 1469 | 5  | Q9V953  | Q9v953 drosophila   |
| 258 | 7 | 2.6 | 395 | 10 | Q65502 | Q65502 arabidopsis  | 331 | 7 | 2.6 | 1530 | 11 | Q9WUG5  | Q9wug5 rattus norv  |
| 259 | 7 | 2.6 | 399 | 5  | Q8T8N3 | Q8t8n3 caenorhabdi  | 332 | 7 | 2.6 | 1778 | 16 | Q8FA32  | Q8fa32 listeria mo  |
| 260 | 7 | 2.6 | 399 | 16 | Q8UEQ8 | Q8ueq8 agrobacteri  | 333 | 7 | 2.6 | 1784 | 12 | Q8Y515  | Q8y515 norwalk vir  |
| 261 | 7 | 2.6 | 399 | 16 | Q8KFR7 | Q8kfr7 chlorobium   | 334 | 7 | 2.6 | 1787 | 12 | Q8JXJ1  | Q8jxj1 norwalk-lik  |
| 262 | 7 | 2.6 | 422 | 5  | Q8SXL8 | Q8sxl8 drosophila   | 335 | 7 | 2.6 | 2691 | 4  | Q8NSJ2  | Q8nsj2 homo sapien  |
| 263 | 7 | 2.6 | 422 | 5  | Q9VVL0 | Q9vvl0 drosophila   | 336 | 7 | 2.6 | 2692 | 4  | Q9Y503  | Q9y503 homo sapien  |
| 264 | 7 | 2.6 | 425 | 17 | Q97W07 | Q97w07 sulfolobus   | 337 | 7 | 2.6 | 2705 | 4  | Q95303  | Q95303 homo sapien  |
| 265 | 7 | 2.6 | 428 | 2  | Q9APH0 | Q9aph0 leptospira   | 338 | 7 | 2.6 | 2725 | 4  | Q9NYE5  | Q9nye5 homo sapien  |
| 266 | 7 | 2.6 | 428 | 16 | Q8F225 | Q8f225 leptospira   | 339 | 6 | 2.2 | 11   | 3  | Q9C1R7  | Q9c1r7 saccharomyc  |
| 267 | 7 | 2.6 | 431 | 16 | Q9RSE0 | Q9rse0 deinococcus  | 340 | 6 | 2.2 | 12   | 3  | Q8J0A7  | Q8j0a7 saccharomyc  |
| 268 | 7 | 2.6 | 436 | 5  | Q95Y86 | Q95y86 caenorhabdi  | 341 | 6 | 2.2 | 16   | 3  | Q8J1R1  | Q8j1r1 saccharomyc  |
| 269 | 7 | 2.6 | 444 | 16 | Q9A4U2 | Q9a4u2 caulobacter  | 342 | 6 | 2.2 | 20   | 3  | Q8J1R0  | Q8j1r0 saccharomyc  |
| 270 | 7 | 2.6 | 451 | 16 | Q9I4N1 | Q9i4n1 pseudomonas  | 343 | 6 | 2.2 | 27   | 12 | Q8QSK5  | Q8qsk5 hepatitis c  |
| 271 | 7 | 2.6 | 462 | 10 | Q8LIC1 | Q8lic1 oryza sativ  | 344 | 6 | 2.2 | 27   | 12 | Q8QSK0  | Q8qsk0 hepatitis c  |
| 272 | 7 | 2.6 | 466 | 16 | Q9PKH7 | Q9pkh7 chlamydia m  | 345 | 6 | 2.2 | 27   | 12 | Q8QSK6  | Q8qsk6 hepatitis c  |
| 273 | 7 | 2.6 | 466 | 16 | Q9K671 | Q9k671 bacillus ha  | 346 | 6 | 2.2 | 27   | 12 | Q8QSK8  | Q8qsk8 hepatitis c  |
| 274 | 7 | 2.6 | 470 | 2  | Q30326 | Q30326 acetobacter  | 347 | 6 | 2.2 | 27   | 12 | Q8QSKJ1 | Q8qskj1 hepatitis c |
| 275 | 7 | 2.6 | 502 | 16 | Q8YB45 | Q8yb45 brucella me  | 348 | 6 | 2.2 | 27   | 12 | Q8QSK3  | Q8qsk3 hepatitis c  |
| 276 | 7 | 2.6 | 502 | 16 | Q8FX93 | Q8fx93 brucella su  | 349 | 6 | 2.2 | 27   | 12 | Q8QSKJ0 | Q8qskj0 hepatitis c |
| 277 | 7 | 2.6 | 515 | 16 | Q9KBJ3 | Q9kbj3 bacillus ha  | 350 | 6 | 2.2 | 27   | 12 | Q8QSK19 | Q8qsk19 hepatitis c |
| 278 | 7 | 2.6 | 519 | 16 | Q8XJ44 | Q8xj44 clostridium  | 351 | 6 | 2.2 | 27   | 12 | Q8QSKJ9 | Q8qskj9 hepatitis c |
| 279 | 7 | 2.6 | 528 | 3  | Q9C2B7 | Q9c2b7 neurospora   | 352 | 6 | 2.2 | 27   | 12 | Q8QSK6  | Q8qsk6 hepatitis c  |
| 280 | 7 | 2.6 | 532 | 10 | Q9LKT4 | Q9lkt4 arabidopsis  | 353 | 6 | 2.2 | 27   | 12 | Q8QSKJ5 | Q8qskj5 hepatitis c |
| 281 | 7 | 2.6 | 533 | 5  | Q8T996 | Q8t996 drosophila   | 354 | 6 | 2.2 | 27   | 12 | Q8QSKJ8 | Q8qskj8 hepatitis c |
| 282 | 7 | 2.6 | 544 | 16 | Q9FCG8 | Q9fcg8 streptomyce  | 355 | 6 | 2.2 | 27   | 12 | Q8QSKJ7 | Q8qskj7 hepatitis c |
| 283 | 7 | 2.6 | 550 | 5  | Q9Y141 | Q9y141 drosophila   | 356 | 6 | 2.2 | 27   | 12 | Q8QSKJ3 | Q8qskj3 hepatitis c |
| 284 | 7 | 2.6 | 554 | 10 | Q9LU28 | Q9lu28 arabidopsis  | 357 | 6 | 2.2 | 27   | 12 | Q8QSK2  | Q8qsk2 hepatitis c  |
| 285 | 7 | 2.6 | 557 | 10 | Q9FEB7 | Q9feb7 oryza sativ  | 358 | 6 | 2.2 | 27   | 12 | Q8QSKJ4 | Q8qskj4 hepatitis c |
| 286 | 7 | 2.6 | 564 | 10 | Q8RXV6 | Q8rxv6 arabidopsis  | 359 | 6 | 2.2 | 27   | 12 | Q8QSKJ2 | Q8qskj2 hepatitis c |
| 287 | 7 | 2.6 | 571 | 16 | Q8ZLH0 | Q8zlh0 salmonella   | 360 | 6 | 2.2 | 28   | 11 | Q9QXB4  | Q9qxb4 mus musculu  |
| 288 | 7 | 2.6 | 586 | 16 | Q98LB3 | Q98lb3 rhizobium l  | 361 | 6 | 2.2 | 33   | 12 | Q72996  | Q72996 hepatitis c  |
| 289 | 7 | 2.6 | 592 | 4  | Q9UJT2 | Q9ujt2 homo sapien  | 362 | 6 | 2.2 | 33   | 12 | Q72995  | Q72995 hepatitis c  |
| 290 | 7 | 2.6 | 601 | 16 | Q9HYI2 | Q9hyi2 pseudomonas  | 363 | 6 | 2.2 | 33   | 12 | Q72997  | Q72997 hepatitis c  |
| 291 | 7 | 2.6 | 609 | 3  | Q9HFY2 | Q9hfi2 neurospora   | 364 | 6 | 2.2 | 33   | 12 | Q72999  | Q72999 hepatitis c  |
| 292 | 7 | 2.6 | 634 | 5  | Q9V978 | Q9v978 drosophila   | 365 | 6 | 2.2 | 33   | 12 | Q72998  | Q72998 hepatitis c  |
| 293 | 7 | 2.6 | 634 | 5  | Q44116 | Q44116 drosophila   | 366 | 6 | 2.2 | 33   | 12 | Q72994  | Q72994 hepatitis c  |
| 294 | 7 | 2.6 | 643 | 2  | Q68085 | Q68085 rhodobacter  | 367 | 6 | 2.2 | 33   | 12 | Q73007  | Q73007 hepatitis c  |
| 295 | 7 | 2.6 | 659 | 16 | Q9FTU7 | Q9ftu7 corynebacte  | 368 | 6 | 2.2 | 33   | 12 | Q73004  | Q73004 hepatitis c  |
| 296 | 7 | 2.6 | 677 | 10 | Q9FNB7 | Q9fnb7 arabidopsis  | 369 | 6 | 2.2 | 36   | 2  | Q9R4X9  | Q9r4x9 azotobacter  |
| 297 | 7 | 2.6 | 679 | 10 | Q8GY46 | Q8gy46 arabidopsis  | 370 | 6 | 2.2 | 37   | 2  | Q8KKA8  | Q8kka8 proteus vul  |
| 298 | 7 | 2.6 | 693 | 10 | Q9FTM8 | Q9ftm8 arabidopsis  | 371 | 6 | 2.2 | 40   | 12 | Q91K62  | Q91k62 hepatitis c  |
| 299 | 7 | 2.6 | 717 | 16 | Q92NM8 | Q92nm8 rhizobium m  | 372 | 6 | 2.2 | 41   | 16 | Q987D0  | Q987d0 rhizobium l  |
| 300 | 7 | 2.6 | 724 | 16 | Q8UDN9 | Q8udn9 agrobacteri  | 373 | 6 | 2.2 | 43   | 6  | Q9XSR9  | Q9xsr9 canis famil  |
| 301 | 7 | 2.6 | 790 | 2  | Q9X285 | Q9x285 pantoea cit  | 374 | 6 | 2.2 | 45   | 12 | Q9PRQ4  | Q9prq4 hepatitis c  |
| 302 | 7 | 2.6 | 792 | 16 | Q8GIM8 | Q8gim8 brucella su  | 375 | 6 | 2.2 | 46   | 17 | Q8U113  | Q8u113 pyrococcus   |
| 303 | 7 | 2.6 | 796 | 16 | Q8ZRS1 | Q8zrs1 salmonella   | 376 | 6 | 2.2 | 47   | 12 | Q9QK97  | Q9qk97 rift valley  |
| 304 | 7 | 2.6 | 796 | 16 | Q8Z9E0 | Q8z9e0 salmonella   | 377 | 6 | 2.2 | 47   | 12 | Q9QK94  | Q9qk94 rift valley  |
| 305 | 7 | 2.6 | 796 | 16 | Q8X946 | Q8x946 escherichia  | 378 | 6 | 2.2 | 47   | 12 | Q9QK90  | Q9qk90 rift valley  |
| 306 | 7 | 2.6 | 797 | 16 | Q8Y9G6 | Q8y9g6 brucella me  | 379 | 6 | 2.2 | 47   | 12 | Q9QK93  | Q9qk93 rift valley  |
| 307 | 7 | 2.6 | 802 | 16 | Q8FL38 | Q8fl38 escherichia  | 380 | 6 | 2.2 | 47   | 12 | Q9QKA0  | Q9qka0 rift valley  |
| 308 | 7 | 2.6 | 823 | 16 | Q8X287 | Q8x287 escherichia  | 381 | 6 | 2.2 | 47   | 12 | Q9QK96  | Q9qk96 rift valley  |

|     |   |     |    |    |        |                     |     |   |     |     |    |        |                     |
|-----|---|-----|----|----|--------|---------------------|-----|---|-----|-----|----|--------|---------------------|
| 382 | 6 | 2.2 | 47 | 12 | Q9QK99 | Q9QK99 rift valley  | 455 | 6 | 2.2 | 85  | 12 | Q84996 | Q84996 porcine rep  |
| 383 | 6 | 2.2 | 47 | 12 | Q9QK98 | Q9QK98 rift valley  | 456 | 6 | 2.2 | 85  | 12 | Q84990 | Q84990 porcine rep  |
| 384 | 6 | 2.2 | 47 | 12 | Q9QK95 | Q9QK95 rift valley  | 457 | 6 | 2.2 | 85  | 12 | Q84988 | Q84988 porcine rep  |
| 385 | 6 | 2.2 | 47 | 12 | Q9QK88 | Q9QK88 rift valley  | 458 | 6 | 2.2 | 85  | 12 | Q84994 | Q84994 porcine rep  |
| 386 | 6 | 2.2 | 47 | 12 | Q9QK92 | Q9QK92 rift valley  | 459 | 6 | 2.2 | 85  | 12 | Q84985 | Q84985 porcine rep  |
| 387 | 6 | 2.2 | 47 | 12 | Q9QK89 | Q9QK89 rift valley  | 460 | 6 | 2.2 | 85  | 12 | Q84992 | Q84992 porcine rep  |
| 388 | 6 | 2.2 | 47 | 12 | Q9QK82 | Q9QK82 rift valley  | 461 | 6 | 2.2 | 85  | 12 | Q84991 | Q84991 porcine rep  |
| 389 | 6 | 2.2 | 47 | 12 | Q9QK91 | Q9QK91 rift valley  | 462 | 6 | 2.2 | 85  | 12 | Q84998 | Q84998 porcine rep  |
| 390 | 6 | 2.2 | 47 | 12 | Q9QK91 | Q9QK91 rift valley  | 463 | 6 | 2.2 | 85  | 12 | Q84993 | Q84993 porcine rep  |
| 391 | 6 | 2.2 | 47 | 12 | Q9QK91 | Q9QK91 rift valley  | 464 | 6 | 2.2 | 85  | 12 | Q84987 | Q84987 porcine rep  |
| 392 | 6 | 2.2 | 48 | 12 | Q9QK83 | Q9QK83 rift valley  | 465 | 6 | 2.2 | 85  | 12 | Q84989 | Q84989 porcine rep  |
| 393 | 6 | 2.2 | 50 | 12 | Q9J111 | Q9J111 hepatitis c  | 466 | 6 | 2.2 | 85  | 12 | Q84995 | Q84995 porcine rep  |
| 394 | 6 | 2.2 | 51 | 8  | Q9Z2V8 | Q9Z2V8 saccharomyc  | 467 | 6 | 2.2 | 85  | 12 | Q84995 | Q84995 porcine rep  |
| 395 | 6 | 2.2 | 56 | 5  | Q8IF31 | Q8IF31 trypanosoma  | 468 | 6 | 2.2 | 85  | 16 | Q914A5 | Q914A5 pseudomonas  |
| 396 | 6 | 2.2 | 57 | 16 | Q8U595 | Q8U595 caenorhabdi  | 469 | 6 | 2.2 | 85  | 16 | Q8K7Q7 | Q8K7Q7 streptococ   |
| 397 | 6 | 2.2 | 57 | 16 | Q8U595 | Q8U595 agrobacteri  | 470 | 6 | 2.2 | 87  | 2  | Q44954 | Q44954 bacillus br  |
| 398 | 6 | 2.2 | 60 | 16 | Q93J10 | Q93J10 streptomyc   | 471 | 6 | 2.2 | 87  | 10 | Q9SPC3 | Q9SPC3 brassica ol  |
| 399 | 6 | 2.2 | 64 | 12 | Q8U287 | Q8U287 garlic late  | 472 | 6 | 2.2 | 87  | 10 | Q9AXV7 | Q9AXV7 brassica ol  |
| 400 | 6 | 2.2 | 65 | 16 | Q8RD40 | Q8RD40 thermoanser  | 473 | 6 | 2.2 | 87  | 10 | Q9SPC6 | Q9SPC6 brassica na  |
| 401 | 6 | 2.2 | 66 | 10 | Q9X1Z7 | Q9X1Z7 oryza sativ  | 474 | 6 | 2.2 | 88  | 10 | Q9SPC7 | Q9SPC7 brassica na  |
| 402 | 6 | 2.2 | 66 | 16 | Q9PFW1 | Q9PFW1 xyelliafas   | 475 | 6 | 2.2 | 88  | 10 | Q9SPC4 | Q9SPC4 brassica na  |
| 403 | 6 | 2.2 | 67 | 7  | Q31588 | Q31588 salmo salar  | 476 | 6 | 2.2 | 89  | 10 | Q9SPC0 | Q9SPC0 brassica ca  |
| 404 | 6 | 2.2 | 67 | 7  | Q31582 | Q31582 salmo salar  | 477 | 6 | 2.2 | 89  | 10 | Q9SPC1 | Q9SPC1 brassica ol  |
| 405 | 6 | 2.2 | 67 | 7  | Q31577 | Q31577 salmo salar  | 478 | 6 | 2.2 | 89  | 10 | Q9SPC5 | Q9SPC5 brassica na  |
| 406 | 6 | 2.2 | 67 | 7  | Q31581 | Q31581 salmo salar  | 479 | 6 | 2.2 | 90  | 2  | Q3CDB1 | Q3CDB1 staphylococ  |
| 407 | 6 | 2.2 | 67 | 7  | Q31580 | Q31580 salmo salar  | 480 | 6 | 2.2 | 90  | 10 | Q8RQ00 | Q8RQ00 oryza sativ  |
| 408 | 6 | 2.2 | 67 | 7  | Q31578 | Q31578 salmo salar  | 481 | 6 | 2.2 | 92  | 5  | Q8IG50 | Q8IG50 drosophila   |
| 409 | 6 | 2.2 | 67 | 7  | Q31578 | Q31578 salmo salar  | 482 | 6 | 2.2 | 92  | 10 | Q8W213 | Q8W213 setaria ita  |
| 410 | 6 | 2.2 | 67 | 7  | Q31583 | Q31583 salmo salar  | 483 | 6 | 2.2 | 92  | 11 | Q8BNE5 | Q8BNE5 mus musculus |
| 411 | 6 | 2.2 | 68 | 2  | Q8GR82 | Q8GR82 thermus the  | 484 | 6 | 2.2 | 92  | 11 | Q8X2Q4 | Q8X2Q4 escherichia  |
| 412 | 6 | 2.2 | 69 | 4  | Q8BST5 | Q8BST5 homo sapien  | 485 | 6 | 2.2 | 92  | 16 | Q8X2Q4 | Q8X2Q4 pyrobaculum  |
| 413 | 6 | 2.2 | 70 | 17 | Q8Q017 | Q8Q017 methanosarc  | 486 | 6 | 2.2 | 94  | 17 | Q8ZUG0 | Q8ZUG0 pyrobaculum  |
| 414 | 6 | 2.2 | 71 | 2  | Q8AE14 | Q8AE14 acetobacter  | 487 | 6 | 2.2 | 95  | 9  | Q8AZL0 | Q8AZL0 bacterioph   |
| 415 | 6 | 2.2 | 71 | 4  | Q8IXY0 | Q8IXY0 homo sapien  | 488 | 6 | 2.2 | 95  | 9  | Q38322 | Q38322 lactococcus  |
| 416 | 6 | 2.2 | 71 | 11 | Q8K2X8 | Q8K2X8 mus musculus | 489 | 6 | 2.2 | 95  | 16 | Q9C183 | Q9C183 lactococcus  |
| 417 | 6 | 2.2 | 71 | 11 | Q8BT75 | Q8BT75 mus musculus | 490 | 6 | 2.2 | 96  | 16 | Q8F4F7 | Q8F4F7 leptospira   |
| 418 | 6 | 2.2 | 72 | 16 | Q8U739 | Q8U739 mycobacteri  | 491 | 6 | 2.2 | 97  | 16 | Q8CKC3 | Q8CKC3 yersinia pe  |
| 419 | 6 | 2.2 | 72 | 16 | Q8U739 | Q8U739 mycobacteri  | 492 | 6 | 2.2 | 98  | 10 | Q9AWA3 | Q9AWA3 beta vulgar  |
| 420 | 6 | 2.2 | 73 | 2  | Q56009 | Q56009 synchococ    | 493 | 6 | 2.2 | 99  | 16 | Q8UG52 | Q8UG52 agrobacteri  |
| 421 | 6 | 2.2 | 75 | 16 | Q8D5V4 | Q8D5V4 vibrio vuln  | 494 | 6 | 2.2 | 100 | 10 | Q8W2X0 | Q8W2X0 oryza sativ  |
| 422 | 6 | 2.2 | 77 | 10 | Q8RX41 | Q8RX41 hordeum vul  | 495 | 6 | 2.2 | 101 | 10 | Q8H8S4 | Q8H8S4 oryza sativ  |
| 423 | 6 | 2.2 | 77 | 10 | Q8RX44 | Q8RX44 hordeum chi  | 496 | 6 | 2.2 | 102 | 8  | Q8LUC3 | Q8LUC3 phrynoceph   |
| 424 | 6 | 2.2 | 77 | 10 | Q8RX43 | Q8RX43 hordeum mur  | 497 | 6 | 2.2 | 102 | 8  | Q8LUC3 | Q8LUC3 phrynoceph   |
| 425 | 6 | 2.2 | 77 | 10 | Q8RX42 | Q8RX42 hordeum mur  | 498 | 6 | 2.2 | 103 | 5  | Q8LUC3 | Q8LUC3 phrynoceph   |
| 426 | 6 | 2.2 | 77 | 10 | Q8RX40 | Q8RX40 hordeum spo  | 499 | 6 | 2.2 | 103 | 5  | Q8LUC3 | Q8LUC3 phrynoceph   |
| 427 | 6 | 2.2 | 77 | 10 | Q8RX48 | Q8RX48 hordeum bre  | 500 | 6 | 2.2 | 103 | 17 | Q9YD43 | Q9YD43 aeropyrum p  |
| 428 | 6 | 2.2 | 78 | 4  | Q8LVC9 | Q8LVC9 homo sapien  | 501 | 6 | 2.2 | 103 | 17 | Q9YD43 | Q9YD43 aeropyrum p  |
| 429 | 6 | 2.2 | 78 | 10 | Q8RX46 | Q8RX46 hordeum bul  | 502 | 6 | 2.2 | 104 | 16 | F73113 | F73113 synchocyst   |
| 430 | 6 | 2.2 | 78 | 10 | Q8RX49 | Q8RX49 hordeum bre  | 503 | 6 | 2.2 | 104 | 16 | F73113 | F73113 synchocyst   |
| 431 | 6 | 2.2 | 78 | 10 | Q8RX47 | Q8RX47 hordeum jub  | 504 | 6 | 2.2 | 104 | 16 | F73113 | F73113 synchocyst   |
| 432 | 6 | 2.2 | 78 | 10 | Q8RX45 | Q8RX45 hordeum bul  | 505 | 6 | 2.2 | 105 | 16 | Q8P215 | Q8P215 streptococ   |
| 433 | 6 | 2.2 | 81 | 16 | Q9K5U4 | Q9K5U4 bacillus ha  | 506 | 6 | 2.2 | 105 | 17 | Q96ZL4 | Q96ZL4 sulfolobus   |
| 434 | 6 | 2.2 | 81 | 16 | Q8UIX6 | Q8UIX6 agrobacteri  | 507 | 6 | 2.2 | 107 | 11 | Q8CK88 | Q8CK88 mus musculus |
| 435 | 6 | 2.2 | 83 | 10 | Q42023 | Q42023 arabidopsis  | 508 | 6 | 2.2 | 107 | 16 | Q8KDF1 | Q8KDF1 chlorobium   |
| 436 | 6 | 2.2 | 83 | 12 | Q8QV22 | Q8QV22 avian reovi  | 509 | 6 | 2.2 | 107 | 17 | Q9Y8L9 | Q9Y8L9 aeropyrum p  |
| 437 | 6 | 2.2 | 83 | 12 | Q8QV33 | Q8QV33 avian reovi  | 510 | 6 | 2.2 | 107 | 17 | Q9Y8L9 | Q9Y8L9 aeropyrum p  |
| 438 | 6 | 2.2 | 84 | 11 | Q98B02 | Q98B02 rhizobium l  | 511 | 6 | 2.2 | 108 | 5  | Q61383 | Q61383 papilio gla  |
| 439 | 6 | 2.2 | 84 | 16 | Q8BFW2 | Q8BFW2 mus musculus | 512 | 6 | 2.2 | 109 | 5  | Q8MR57 | Q8MR57 drosophila   |
| 440 | 6 | 2.2 | 84 | 16 | Q8P186 | Q8P186 xanthomonas  | 513 | 6 | 2.2 | 110 | 5  | Q43362 | Q43362 chlamydia t  |
| 441 | 6 | 2.2 | 84 | 16 | Q8DFY3 | Q8DFY3 vibrio vuln  | 514 | 6 | 2.2 | 112 | 5  | Q43362 | Q43362 chlamydia t  |
| 442 | 6 | 2.2 | 85 | 7  | Q95HX8 | Q95HX8 salmo salar  | 515 | 6 | 2.2 | 112 | 10 | Q9FYR1 | Q9FYR1 arabidopsis  |
| 443 | 6 | 2.2 | 85 | 7  | Q95IS0 | Q95IS0 salmo salar  | 516 | 6 | 2.2 | 112 | 12 | Q65509 | Q65509 barmah fore  |
| 444 | 6 | 2.2 | 85 | 7  | Q95IS6 | Q95IS6 salmo salar  | 517 | 6 | 2.2 | 113 | 16 | Q92N79 | Q92N79 rhizobium m  |
| 445 | 6 | 2.2 | 85 | 7  | Q95HX5 | Q95HX5 salmo salar  | 518 | 6 | 2.2 | 113 | 16 | Q95J66 | Q95J66 pan troglod  |
| 446 | 6 | 2.2 | 85 | 7  | Q95IS8 | Q95IS8 salmo salar  | 519 | 6 | 2.2 | 114 | 16 | Q95J66 | Q95J66 pan troglod  |
| 447 | 6 | 2.2 | 85 | 7  | Q95HX2 | Q95HX2 salmo salar  | 520 | 6 | 2.2 | 114 | 16 | Q95J66 | Q95J66 pan troglod  |
| 448 | 6 | 2.2 | 85 | 7  | Q95IS2 | Q95IS2 salmo salar  | 521 | 6 | 2.2 | 115 | 17 | Q9HIG9 | Q9HIG9 thermoplas   |
| 449 | 6 | 2.2 | 85 | 7  | Q95HX3 | Q95HX3 salmo salar  | 522 | 6 | 2.2 | 115 | 17 | Q9HIG9 | Q9HIG9 thermoplas   |
| 450 | 6 | 2.2 | 85 | 7  | Q95HX6 | Q95HX6 salmo salar  | 523 | 6 | 2.2 | 117 | 10 | Q9X5G6 | Q9X5G6 tortula rur  |
| 451 | 6 | 2.2 | 85 | 7  | Q95IS5 | Q95IS5 salmo salar  | 524 | 6 | 2.2 | 118 | 10 | Q9ZRE0 | Q9ZRE0 nicotiana t  |
| 452 | 6 | 2.2 | 85 | 10 | Q9AXY6 | Q9AXY6 brassica ol  | 525 | 6 | 2.2 | 118 | 12 | Q86753 | Q86753 hepatitis c  |
| 453 | 6 | 2.2 | 85 | 10 | Q9SPC2 | Q9SPC2 brassica ol  | 526 | 6 | 2.2 | 118 | 16 | Q9RYP1 | Q9RYP1 deinococcus  |
| 454 | 6 | 2.2 | 85 | 12 | Q84997 | Q84997 porcine rep  | 527 | 6 | 2.2 | 119 | 16 | Q8NMRE | Q8NMRE corynebacte  |
| 455 | 6 | 2.2 | 85 | 12 | Q84986 | Q84986 porcine rep  | 527 | 6 | 2.2 | 119 | 9  | Q8SCR4 | Q8SCR4 pseudomonas  |



|     |   |     |     |    |         |                      |     |   |     |     |    |        |                       |
|-----|---|-----|-----|----|---------|----------------------|-----|---|-----|-----|----|--------|-----------------------|
| 528 | 6 | 2.2 | 119 | 17 | Q8U0N0  | Q8u0n0 pyrococcus    | 601 | 6 | 2.2 | 130 | 17 | Q9YD79 | Q9yd79 aeropyrum p    |
| 529 | 6 | 2.2 | 120 | 6  | Q8HY50  | Q8hy50 oryctolagus   | 602 | 6 | 2.2 | 132 | 10 | Q9FUI9 | Q9fui9 rubus idaeu    |
| 530 | 6 | 2.2 | 120 | 10 | Q9AT96  | Q9at96 brassica ca   | 603 | 6 | 2.2 | 132 | 16 | Q8DS27 | Q8ds27 streptococ     |
| 531 | 6 | 2.2 | 120 | 11 | Q8C8D4  | Q8c8d4 mus musculu   | 604 | 6 | 2.2 | 133 | 2  | Q8KVS3 | Q8kvs3 renibacteri    |
| 532 | 6 | 2.2 | 120 | 12 | Q67426  | Q67426 dengue viru   | 605 | 6 | 2.2 | 133 | 2  | Q8KVS2 | Q8kvs2 renibacteri    |
| 533 | 6 | 2.2 | 120 | 16 | Q8UD03  | Q8ud03 agrobacteri   | 606 | 6 | 2.2 | 133 | 16 | Q922J1 | Q922j1 rhizobium m    |
| 534 | 6 | 2.2 | 121 | 5  | Q95SM4  | Q95sm4 drosophila    | 607 | 6 | 2.2 | 133 | 17 | Q9YDU6 | Q9ydu6 aeropyrum p    |
| 535 | 6 | 2.2 | 122 | 11 | Q9D105  | Q9d105 mus musculu   | 608 | 6 | 2.2 | 133 | 17 | Q9Y928 | Q9y928 aeropyrum p    |
| 536 | 6 | 2.2 | 123 | 2  | Q8GQ77  | Q8gq77 pseudomonas   | 609 | 6 | 2.2 | 134 | 17 | Q8YKA3 | Q8yka3 anabaena sp    |
| 537 | 6 | 2.2 | 123 | 10 | Q9LVR8  | Q9lvr8 arabisidopsis | 610 | 6 | 2.2 | 134 | 17 | Q8YKA3 | Q8yka3 anabaena sp    |
| 538 | 6 | 2.2 | 123 | 10 | Q9XFM3  | Q9xfm3 dianthus ca   | 611 | 6 | 2.2 | 136 | 2  | Q33299 | Q33299 pyrococcus     |
| 539 | 6 | 2.2 | 123 | 16 | Q9JUQ2  | Q9jqz2 neisseria m   | 612 | 6 | 2.2 | 136 | 10 | Q9FX60 | Q9fx60 arabisidopsis  |
| 540 | 6 | 2.2 | 123 | 16 | Q99Z15  | Q99z15 streptococ    | 613 | 6 | 2.2 | 136 | 10 | Q8LCA8 | Q8lca8 arabisidopsis  |
| 541 | 6 | 2.2 | 123 | 16 | Q8K6W0  | Q8k6w0 streptococ    | 614 | 6 | 2.2 | 136 | 10 | Q8SA80 | Q8sa80 oryza sativ    |
| 542 | 6 | 2.2 | 124 | 2  | Q9X563  | Q9x563 enterococcu   | 615 | 6 | 2.2 | 137 | 10 | Q9FX17 | Q9fxi17 arabisidopsis |
| 543 | 6 | 2.2 | 124 | 17 | Q8Q0M4  | Q8q0m4 methanosaer   | 616 | 6 | 2.2 | 137 | 12 | Q65517 | Q65517 barnah fore    |
| 544 | 6 | 2.2 | 125 | 17 | Q97WY5  | Q97wy5 sulfobacte    | 617 | 6 | 2.2 | 137 | 17 | Q82267 | Q82267 archaeoglob    |
| 545 | 6 | 2.2 | 126 | 2  | P94825  | P94825 helicobacte   | 618 | 6 | 2.2 | 138 | 4  | Q9NVU8 | Q9nvu8 homo sapien    |
| 546 | 6 | 2.2 | 126 | 5  | Q9IBH3  | Q9ibh3 plasmodium    | 619 | 6 | 2.2 | 140 | 12 | Q65520 | Q65520 barnah fore    |
| 547 | 6 | 2.2 | 126 | 9  | Q9T125  | Q9t125 staphylococ   | 620 | 6 | 2.2 | 141 | 4  | Q8TEG2 | Q8teg2 homo sapien    |
| 548 | 6 | 2.2 | 126 | 10 | Q9FZFF5 | Q9fzf5 arabisidopsis | 621 | 6 | 2.2 | 141 | 11 | Q9DCL1 | Q9dcl1 mus musculu    |
| 549 | 6 | 2.2 | 126 | 16 | Q9RMQ5  | Q9rmq5 vibrio chol   | 622 | 6 | 2.2 | 141 | 12 | Q65500 | Q65500 barnah fore    |
| 550 | 6 | 2.2 | 126 | 16 | Q99SQ0  | Q99sq0 staphylococ   | 623 | 6 | 2.2 | 141 | 12 | Q65505 | Q65505 barnah fore    |
| 551 | 6 | 2.2 | 126 | 16 | Q97RV8  | Q97rv8 streptococ    | 624 | 6 | 2.2 | 141 | 12 | Q65498 | Q65498 barnah fore    |
| 552 | 6 | 2.2 | 126 | 16 | Q9ZLU3  | Q9zlu3 helicobacte   | 625 | 6 | 2.2 | 141 | 12 | Q65504 | Q65504 barnah fore    |
| 553 | 6 | 2.2 | 126 | 16 | Q8DQM7  | Q8dqm7 streptococ    | 626 | 6 | 2.2 | 141 | 12 | Q65497 | Q65497 barnah fore    |
| 554 | 6 | 2.2 | 127 | 10 | Q43202  | Q43202 triticum ae   | 627 | 6 | 2.2 | 141 | 12 | Q65507 | Q65507 barnah fore    |
| 555 | 6 | 2.2 | 127 | 10 | Q42832  | Q42832 hordeum vul   | 628 | 6 | 2.2 | 141 | 12 | Q65506 | Q65506 barnah fore    |
| 556 | 6 | 2.2 | 127 | 10 | Q43303  | Q43303 glycine max   | 629 | 6 | 2.2 | 141 | 12 | Q65521 | Q65521 barnah fore    |
| 557 | 6 | 2.2 | 127 | 10 | Q43203  | Q43203 triticum ae   | 630 | 6 | 2.2 | 141 | 12 | Q65499 | Q65499 barnah fore    |
| 558 | 6 | 2.2 | 127 | 10 | Q42782  | Q42782 glycine max   | 631 | 6 | 2.2 | 141 | 12 | Q65508 | Q65508 barnah fore    |
| 559 | 6 | 2.2 | 127 | 10 | P94019  | P94019 medicago sa   | 632 | 6 | 2.2 | 141 | 12 | Q65516 | Q65516 barnah fore    |
| 560 | 6 | 2.2 | 127 | 16 | Q8D4D5  | Q8d4d5 vibrio vuln   | 633 | 6 | 2.2 | 141 | 16 | Q8DWI3 | Q8dwi3 streptococ     |
| 561 | 6 | 2.2 | 127 | 17 | Q27570  | Q27570 methanobact   | 634 | 6 | 2.2 | 142 | 5  | Q22586 | Q22586 caenorhabdi    |
| 562 | 6 | 2.2 | 128 | 5  | Q95W53  | Q95w53 haemophilu    | 635 | 6 | 2.2 | 142 | 12 | Q65524 | Q65524 barnah fore    |
| 563 | 6 | 2.2 | 128 | 11 | Q8V112  | Q8v112 rattus norv   | 636 | 6 | 2.2 | 142 | 12 | Q41146 | Q41146 parametium     |
| 564 | 6 | 2.2 | 128 | 11 | Q9DAN8  | Q9dan8 mus musculu   | 637 | 6 | 2.2 | 142 | 17 | Q8TV53 | Q8tv53 methanopyru    |
| 565 | 6 | 2.2 | 128 | 12 | Q57006  | Q57006 porcine rep   | 638 | 6 | 2.2 | 143 | 2  | Q9AEW2 | Q9aew2 pseudomonas    |
| 566 | 6 | 2.2 | 128 | 12 | Q91H98  | Q91h98 porcine rep   | 639 | 6 | 2.2 | 143 | 5  | Q9GNF3 | Q9gnf3 leishmania     |
| 567 | 6 | 2.2 | 128 | 12 | Q9DH72  | Q9dh72 porcine rep   | 640 | 6 | 2.2 | 143 | 12 | Q65519 | Q65519 barnah fore    |
| 568 | 6 | 2.2 | 128 | 12 | Q91H90  | Q91h90 porcine rep   | 641 | 6 | 2.2 | 144 | 1  | Q9UW22 | Q9uw22 sulfobolus     |
| 569 | 6 | 2.2 | 128 | 12 | Q91HA1  | Q91ha1 porcine rep   | 642 | 6 | 2.2 | 144 | 12 | Q65522 | Q65522 barnah fore    |
| 570 | 6 | 2.2 | 128 | 12 | Q91OG3  | Q91og3 porcine rep   | 643 | 6 | 2.2 | 144 | 12 | Q83081 | Q83081 lynchis rin    |
| 571 | 6 | 2.2 | 128 | 12 | Q91HA3  | Q91ha3 porcine rep   | 644 | 6 | 2.2 | 144 | 17 | Q8ZVQ5 | Q8zvg5 pyrobaculum    |
| 572 | 6 | 2.2 | 128 | 12 | Q91OS5  | Q91os5 porcine rep   | 645 | 6 | 2.2 | 146 | 2  | Q93P93 | Q93p93 microscilla    |
| 573 | 6 | 2.2 | 128 | 12 | Q91H91  | Q91h91 porcine rep   | 646 | 6 | 2.2 | 146 | 2  | Q33548 | Q33548 rhodobacter    |
| 574 | 6 | 2.2 | 128 | 12 | Q8JNL6  | Q8jnl6 porcine rep   | 647 | 6 | 2.2 | 146 | 11 | Q9DAB9 | Q9dab9 mus musculu    |
| 575 | 6 | 2.2 | 128 | 12 | Q91H89  | Q91h89 porcine rep   | 648 | 6 | 2.2 | 146 | 12 | Q65523 | Q65523 barnah fore    |
| 576 | 6 | 2.2 | 128 | 12 | Q85023  | Q85023 porcine rep   | 649 | 6 | 2.2 | 146 | 12 | Q65503 | Q65503 barnah fore    |
| 577 | 6 | 2.2 | 128 | 12 | Q57005  | Q57005 porcine rep   | 650 | 6 | 2.2 | 146 | 12 | Q9EP31 | Q9ep31 hepatitis c    |
| 578 | 6 | 2.2 | 128 | 12 | Q91H96  | Q91h96 porcine rep   | 651 | 6 | 2.2 | 147 | 16 | Q8ETG9 | Q8etg9 oceanobacil    |
| 579 | 6 | 2.2 | 128 | 12 | Q91H97  | Q91h97 porcine rep   | 652 | 6 | 2.2 | 148 | 4  | Q9H128 | Q9h128 homo sapien    |
| 580 | 6 | 2.2 | 128 | 12 | Q91HA2  | Q91ha2 porcine rep   | 653 | 6 | 2.2 | 148 | 8  | Q9G8Q7 | Q9g8q7 naegleria g    |
| 581 | 6 | 2.2 | 128 | 12 | Q85017  | Q85017 porcine rep   | 654 | 6 | 2.2 | 148 | 16 | Q65941 | Q65941 escherichia    |
| 582 | 6 | 2.2 | 128 | 12 | Q91H99  | Q91h99 porcine rep   | 655 | 6 | 2.2 | 148 | 16 | Q9KZ19 | Q9kz19 streptomyc     |
| 583 | 6 | 2.2 | 128 | 12 | Q9DPB6  | Q9dpb6 porcine rep   | 656 | 6 | 2.2 | 149 | 11 | Q8BNE8 | Q8bne8 mus musculu    |
| 584 | 6 | 2.2 | 128 | 12 | Q9DPB7  | Q9dpb7 porcine rep   | 657 | 6 | 2.2 | 149 | 12 | Q65518 | Q65518 barnah fore    |
| 585 | 6 | 2.2 | 128 | 12 | Q91H95  | Q91h95 porcine rep   | 658 | 6 | 2.2 | 150 | 2  | Q8KR62 | Q8kr62 escherichia    |
| 586 | 6 | 2.2 | 128 | 12 | Q57004  | Q57004 porcine rep   | 659 | 6 | 2.2 | 150 | 16 | Q9AAK2 | Q9aak2 caulobacter    |
| 587 | 6 | 2.2 | 128 | 12 | Q8JNM2  | Q8jnm2 porcine rep   | 660 | 6 | 2.2 | 150 | 16 | Q981L8 | Q981l8 rhizobium l    |
| 588 | 6 | 2.2 | 128 | 12 | Q9WJRO  | Q9wjro porcine rep   | 661 | 6 | 2.2 | 150 | 16 | Q8G6R4 | Q8g6r4 bifidobacte    |
| 589 | 6 | 2.2 | 128 | 12 | Q93162  | Q93162 porcine rep   | 662 | 6 | 2.2 | 151 | 5  | P91717 | P91717 dugesia tig    |
| 590 | 6 | 2.2 | 128 | 12 | Q91H86  | Q91h86 porcine rep   | 663 | 6 | 2.2 | 152 | 10 | Q9FE54 | Q9fe54 arabisidopsis  |
| 591 | 6 | 2.2 | 128 | 12 | Q55480  | Q55480 porcine rep   | 664 | 6 | 2.2 | 152 | 10 | Q94E63 | Q94e63 oryza sativ    |
| 592 | 6 | 2.2 | 128 | 12 | Q91OG7  | Q91og7 porcine rep   | 665 | 6 | 2.2 | 152 | 16 | Q8YWH3 | Q8ywh3 anabaena sp    |
| 593 | 6 | 2.2 | 128 | 12 | Q91H85  | Q91h85 porcine rep   | 666 | 6 | 2.2 | 152 | 17 | Q8YWH3 | Q8ywh3 anabaena sp    |
| 594 | 6 | 2.2 | 128 | 12 | Q91H93  | Q91h93 porcine rep   | 667 | 6 | 2.2 | 153 | 4  | Q8B7K1 | Q8b7k1 pyrococcus     |
| 595 | 6 | 2.2 | 128 | 12 | Q91H94  | Q91h94 porcine rep   | 668 | 6 | 2.2 | 153 | 5  | Q8N7N1 | Q8n7n1 homo sapien    |
| 596 | 6 | 2.2 | 128 | 12 | Q8BDR9  | Q8bdr9 porcine rep   | 669 | 6 | 2.2 | 153 | 10 | Q9MAK7 | Q9mak7 arabisidopsis  |
| 597 | 6 | 2.2 | 128 | 12 | Q8BDR8  | Q8bdr8 porcine rep   | 670 | 6 | 2.2 | 153 | 12 | Q65501 | Q65501 barnah fore    |
| 598 | 6 | 2.2 | 129 | 8  | Q9B8E7  | Q9b8e7 stylocheiro   | 671 | 6 | 2.2 | 153 | 12 | Q65502 | Q65502 barnah fore    |
| 599 | 6 | 2.2 | 130 | 5  | Q9VJ85  | Q9vj85 drosophila    | 672 | 6 | 2.2 | 153 | 12 | Q65496 | Q65496 barnah fore    |
| 600 | 6 | 2.2 | 130 | 5  | Q810N0  | Q810n0 drosophila    | 673 | 6 | 2.2 | 153 | 16 | Q8EBJ0 | Q8ebj0 shewanella     |

|     |   |     |     |    |        |                    |     |   |     |     |    |        |                     |
|-----|---|-----|-----|----|--------|--------------------|-----|---|-----|-----|----|--------|---------------------|
| 674 | 6 | 2.2 | 154 | 9  | O80237 | O80237 bacterioph  | 747 | 6 | 2.2 | 162 | 16 | O32078 | O32078 bacillus su  |
| 675 | 6 | 2.2 | 154 | 12 | Q916Q6 | Q916q6 hepatitis c | 748 | 6 | 2.2 | 163 | 2  | Q9AM04 | Q9am04 staphylococ  |
| 676 | 6 | 2.2 | 154 | 12 | Q916P4 | Q916p4 hepatitis c | 749 | 6 | 2.2 | 163 | 2  | Q91C46 | Q91c46 staphylococ  |
| 677 | 6 | 2.2 | 154 | 12 | Q916R7 | Q916r7 hepatitis c | 750 | 6 | 2.2 | 163 | 9  | Q8SDJ8 | Q8sdj8 staphylococ  |
| 678 | 6 | 2.2 | 154 | 12 | Q8QQJ5 | Q8qqj5 hepatitis c | 751 | 6 | 2.2 | 163 | 16 | Q99SU7 | Q99su7 staphylococ  |
| 679 | 6 | 2.2 | 154 | 12 | Q916P1 | Q916p1 hepatitis c | 752 | 6 | 2.2 | 163 | 16 | O8NVR2 | O8nvrr2 staphylococ |
| 680 | 6 | 2.2 | 154 | 12 | Q916S3 | Q916s3 hepatitis c | 753 | 6 | 2.2 | 164 | 2  | O8S988 | O8s988 sphingomona  |
| 681 | 6 | 2.2 | 154 | 12 | Q8QQH9 | Q8qqh9 hepatitis c | 754 | 6 | 2.2 | 164 | 2  | O07092 | O07092 escherichia  |
| 682 | 6 | 2.2 | 154 | 12 | Q8QQH9 | Q8qqh9 hepatitis c | 755 | 6 | 2.2 | 164 | 17 | Q97BY5 | Q97by5 thermoplasm  |
| 683 | 6 | 2.2 | 154 | 12 | Q916S7 | Q916s7 hepatitis c | 756 | 6 | 2.2 | 165 | 2  | Q9F8Q1 | Q9f8q1 carboxydoth  |
| 684 | 6 | 2.2 | 154 | 12 | Q916P0 | Q916p0 hepatitis c | 757 | 6 | 2.2 | 165 | 5  | O46217 | O46217 drosophila   |
| 685 | 6 | 2.2 | 154 | 12 | Q916P3 | Q916p3 hepatitis c | 758 | 6 | 2.2 | 167 | 16 | Q9S338 | Q9s338 desulfovibr  |
| 686 | 6 | 2.2 | 154 | 12 | Q916Q7 | Q916q7 hepatitis c | 759 | 6 | 2.2 | 167 | 16 | Q9KM52 | Q9kms2 vibrio chol  |
| 687 | 6 | 2.2 | 154 | 12 | Q916Q7 | Q916q7 hepatitis c | 760 | 6 | 2.2 | 167 | 16 | Q915S9 | Q915s9 pseudomonas  |
| 688 | 6 | 2.2 | 154 | 12 | O8QQI2 | O8qqi2 hepatitis c | 761 | 6 | 2.2 | 168 | 2  | Q9S573 | Q9s573 pseudomonas  |
| 689 | 6 | 2.2 | 154 | 12 | O8QQJ7 | O8qqj7 hepatitis c | 762 | 6 | 2.2 | 168 | 10 | Q9C7S3 | Q9c7s3 arabidopsis  |
| 690 | 6 | 2.2 | 154 | 12 | O916Q7 | O916q7 hepatitis c | 763 | 6 | 2.2 | 168 | 16 | Q9KMS5 | Q9kms5 vibrio chol  |
| 691 | 6 | 2.2 | 154 | 12 | Q916P2 | O916p2 hepatitis c | 764 | 6 | 2.2 | 168 | 17 | Q9UX13 | Q9ux13 xylellobus   |
| 692 | 6 | 2.2 | 154 | 12 | Q916R1 | Q916r1 hepatitis c | 765 | 6 | 2.2 | 169 | 16 | Q9P9Q4 | Q9p9q4 xylella fae  |
| 693 | 6 | 2.2 | 154 | 12 | Q916R2 | Q916r2 hepatitis c | 766 | 6 | 2.2 | 169 | 16 | O8ZJ15 | O8zj15 versinia pe  |
| 694 | 6 | 2.2 | 154 | 12 | Q916S5 | Q916s5 hepatitis c | 767 | 6 | 2.2 | 170 | 2  | Q9RGV5 | Q9rgv5 salmonella   |
| 695 | 6 | 2.2 | 154 | 12 | O8QQI9 | O8qqi9 hepatitis c | 768 | 6 | 2.2 | 170 | 4  | O60615 | O60615 homo sapien  |
| 696 | 6 | 2.2 | 154 | 12 | Q916Q4 | Q916q4 hepatitis c | 769 | 6 | 2.2 | 170 | 4  | O81VJ8 | O81vj8 homo sapien  |
| 697 | 6 | 2.2 | 154 | 12 | O8QQJ4 | O8qqj4 hepatitis c | 770 | 6 | 2.2 | 170 | 10 | O229S7 | O229s7 arabidopsis  |
| 698 | 6 | 2.2 | 154 | 12 | Q916Q8 | Q916q8 hepatitis c | 771 | 6 | 2.2 | 170 | 17 | Q937S2 | Q937s2 pyrobaculum  |
| 699 | 6 | 2.2 | 154 | 12 | Q916Q0 | Q916q0 hepatitis c | 772 | 6 | 2.2 | 172 | 5  | Q9GQ62 | Q9gq62 ctenorhabdi  |
| 700 | 6 | 2.2 | 154 | 12 | Q916Q0 | Q916q0 hepatitis c | 773 | 6 | 2.2 | 172 | 15 | Q99EM2 | Q99em2 human immun  |
| 701 | 6 | 2.2 | 154 | 12 | O8QQI3 | O8qqi3 hepatitis c | 774 | 6 | 2.2 | 172 | 15 | Q99EL6 | Q99el6 rhizobium l  |
| 702 | 6 | 2.2 | 154 | 12 | Q916Q9 | Q916q9 hepatitis c | 775 | 6 | 2.2 | 172 | 16 | Q98EJ1 | Q98ej1 rhizobium l  |
| 703 | 6 | 2.2 | 154 | 12 | Q916R0 | Q916r0 hepatitis c | 776 | 6 | 2.2 | 172 | 16 | Q8D1F3 | Q8dlf3 versinia pe  |
| 704 | 6 | 2.2 | 154 | 12 | Q916Q1 | Q916q1 hepatitis c | 777 | 6 | 2.2 | 172 | 16 | Q8CMX1 | Q8cmx1 staphylococ  |
| 705 | 6 | 2.2 | 154 | 12 | Q916S8 | Q916s8 hepatitis c | 778 | 6 | 2.2 | 173 | 2  | O87662 | O87662 salmonella   |
| 706 | 6 | 2.2 | 154 | 12 | Q916Q2 | Q916q2 hepatitis c | 779 | 6 | 2.2 | 173 | 8  | Q8WGE2 | Q8wge2 raninoides   |
| 707 | 6 | 2.2 | 154 | 12 | Q916R5 | Q916r5 hepatitis c | 780 | 6 | 2.2 | 173 | 16 | O8XXJ2 | O8xxj2 ralatonia s  |
| 708 | 6 | 2.2 | 154 | 12 | O8QQI0 | O8qqi0 hepatitis c | 781 | 6 | 2.2 | 173 | 16 | Q8FMV0 | Q8fmv0 corynebacte  |
| 709 | 6 | 2.2 | 154 | 12 | Q916S4 | Q916s4 hepatitis c | 782 | 6 | 2.2 | 174 | 16 | Q8XRW8 | Q8xrw8 ralatonia s  |
| 710 | 6 | 2.2 | 154 | 12 | O8QQI5 | Q8qqi5 hepatitis c | 783 | 6 | 2.2 | 175 | 4  | Q9UFY2 | Q9ufy2 homo sapien  |
| 711 | 6 | 2.2 | 154 | 12 | Q916R4 | Q916r4 hepatitis c | 784 | 6 | 2.2 | 175 | 10 | Q9LT07 | Q9lt07 arabidopsis  |
| 712 | 6 | 2.2 | 154 | 12 | Q916P9 | Q916p9 hepatitis c | 785 | 6 | 2.2 | 176 | 16 | Q8ZRP9 | Q8zrp9 salmonella   |
| 713 | 6 | 2.2 | 154 | 12 | O8QQI6 | Q8qqi6 hepatitis c | 786 | 6 | 2.2 | 177 | 16 | Q92BU5 | Q92bu5 listeria in  |
| 714 | 6 | 2.2 | 154 | 12 | O8QQI4 | Q8qqi4 hepatitis c | 787 | 6 | 2.2 | 178 | 12 | Q03729 | Q03729 hepatitis c  |
| 715 | 6 | 2.2 | 154 | 12 | O8QQJ2 | O8qqj2 hepatitis c | 788 | 6 | 2.2 | 179 | 16 | Q8YRT7 | Q8yrt7 anabaena sp  |
| 716 | 6 | 2.2 | 154 | 12 | Q916S9 | Q916s9 hepatitis c | 789 | 6 | 2.2 | 179 | 16 | Q8RER4 | Q8rer4 fusobacteri  |
| 717 | 6 | 2.2 | 154 | 12 | Q916R3 | Q916r3 hepatitis c | 790 | 6 | 2.2 | 179 | 16 | Q8KGC4 | Q8kgc4 chlorobium   |
| 718 | 6 | 2.2 | 154 | 12 | Q916R8 | Q916r8 hepatitis c | 791 | 6 | 2.2 | 180 | 2  | Q9RHL6 | Q9rhl6 actinobacil  |
| 719 | 6 | 2.2 | 154 | 12 | Q916R8 | Q916r8 hepatitis c | 792 | 6 | 2.2 | 180 | 2  | O05384 | O05384 actinobacil  |
| 720 | 6 | 2.2 | 154 | 12 | O8QQI1 | O8qqi1 hepatitis c | 793 | 6 | 2.2 | 180 | 2  | O66263 | O66263 actinobacil  |
| 721 | 6 | 2.2 | 154 | 12 | Q916P8 | Q916p8 hepatitis c | 794 | 6 | 2.2 | 180 | 13 | Q90945 | Q90945 xenopus lae  |
| 722 | 6 | 2.2 | 154 | 12 | Q916P5 | Q916p5 hepatitis c | 795 | 6 | 2.2 | 180 | 16 | Q8UJ17 | Q8uj17 agrobacteri  |
| 723 | 6 | 2.2 | 154 | 12 | Q916R6 | Q916r6 hepatitis c | 796 | 6 | 2.2 | 181 | 4  | Q8NA89 | Q8na89 homo sapien  |
| 724 | 6 | 2.2 | 154 | 12 | Q916G5 | Q916g5 hepatitis c | 797 | 6 | 2.2 | 181 | 16 | Q97R45 | Q97r45 streptococ   |
| 725 | 6 | 2.2 | 154 | 12 | O8RMY3 | O8rmy3 methanosarc | 798 | 6 | 2.2 | 181 | 16 | Q8DQ17 | Q8dq17 streptococ   |
| 726 | 6 | 2.2 | 156 | 10 | Q9FIU6 | Q9fiu6 arabidopsis | 799 | 6 | 2.2 | 181 | 17 | O58306 | O58306 pyrococcus   |
| 727 | 6 | 2.2 | 156 | 16 | Q98P70 | Q98p70 rhizobium l | 800 | 6 | 2.2 | 182 | 10 | Q9LHUS | Q9lhus oryza sativ  |
| 728 | 6 | 2.2 | 157 | 3  | Q9UU40 | Q9uu40 schizosacch | 801 | 6 | 2.2 | 183 | 16 | Q9RHT1 | Q9rht1 fusobacteri  |
| 729 | 6 | 2.2 | 158 | 10 | Q9AK76 | Q9ar76 populus tre | 802 | 6 | 2.2 | 184 | 8  | Q8LX03 | Q8lx03 leishmania d |
| 730 | 6 | 2.2 | 158 | 10 | Q9AK77 | Q9ar77 populus tre | 803 | 6 | 2.2 | 185 | 16 | Q8YJ82 | Q8yj82 brucella me  |
| 731 | 6 | 2.2 | 158 | 16 | Q91210 | Q91210 pseudomonas | 804 | 6 | 2.2 | 185 | 16 | Q8RYM0 | Q8rym0 brucella su  |
| 732 | 6 | 2.2 | 159 | 2  | Q44150 | Q44150 anabaena sp | 805 | 6 | 2.2 | 186 | 16 | Q86545 | Q86545 streptomyce  |
| 733 | 6 | 2.2 | 159 | 12 | Q65515 | Q65515 barmah fore | 806 | 6 | 2.2 | 188 | 10 | Q9CS42 | Q9cs42 arabidopsis  |
| 734 | 6 | 2.2 | 159 | 12 | Q65511 | Q65511 barmah fore | 807 | 6 | 2.2 | 189 | 5  | O60965 | O60965 leishmania   |
| 735 | 6 | 2.2 | 159 | 12 | Q65513 | Q65513 barmah fore | 808 | 6 | 2.2 | 189 | 15 | Q8QI14 | Q8qi14 human immun  |
| 736 | 6 | 2.2 | 159 | 12 | Q65512 | Q65512 barmah fore | 809 | 6 | 2.2 | 189 | 16 | Q9HTG2 | Q9htg2 pseudomonas  |
| 737 | 6 | 2.2 | 159 | 12 | Q65514 | Q65514 barmah fore | 810 | 6 | 2.2 | 189 | 16 | Q98G88 | Q98g88 rhizobium l  |
| 738 | 6 | 2.2 | 159 | 12 | Q65510 | Q65510 barmah fore | 811 | 6 | 2.2 | 190 | 5  | Q81LBO | Q81lbo plasmodium   |
| 739 | 6 | 2.2 | 159 | 16 | Q945V2 | Q945v2 caulobacter | 812 | 6 | 2.2 | 190 | 11 | Q8BSF7 | Q8bsf7 mus musculu  |
| 740 | 6 | 2.2 | 160 | 16 | Q8F756 | Q8f756 leptospira  | 813 | 6 | 2.2 | 190 | 12 | Q83062 | Q83062 lettuce mos  |
| 741 | 6 | 2.2 | 160 | 17 | O59505 | O59505 pyrococcus  | 814 | 6 | 2.2 | 190 | 12 | Q83062 | Q83062 lettuce mos  |
| 742 | 6 | 2.2 | 161 | 5  | O44919 | O44919 caenorhabdi | 815 | 6 | 2.2 | 191 | 16 | Q9AC28 | Q9ac28 caulobacter  |
| 743 | 6 | 2.2 | 161 | 10 | Q08198 | Q08198 nicotiana t | 816 | 6 | 2.2 | 193 | 10 | Q8VZ12 | Q8vz12 arabidopsis  |
| 744 | 6 | 2.2 | 161 | 10 | Q94H20 | Q94h20 oryza sativ | 817 | 6 | 2.2 | 193 | 16 | Q8NTH2 | Q8nth2 corynebacte  |
| 745 | 6 | 2.2 | 161 | 16 | Q8Y5S4 | Q8y5s4 listeria mo | 818 | 6 | 2.2 | 194 | 2  | O54653 | O54653 legyonella   |
| 746 | 6 | 2.2 | 162 | 9  | Q38069 | Q38069 bacterioph  | 819 | 6 | 2.2 | 195 | 4  | Q8WYL1 | Q8wyl1 homo sapien  |

|     |   |     |     |    |        |                     |     |   |     |     |    |         |                     |
|-----|---|-----|-----|----|--------|---------------------|-----|---|-----|-----|----|---------|---------------------|
| 820 | 6 | 2.2 | 195 | 4  | Q96H36 | Q96h36 homo sapien  | 893 | 6 | 2.2 | 218 | 16 | Q8F6E9  | Q8f6e9 leptospira   |
| 821 | 6 | 2.2 | 195 | 9  | Q9AZM3 | Q9azm3 bacterioph   | 894 | 6 | 2.2 | 219 | 5  | Q8MUT9  | Q8mut9 aplysia cal  |
| 822 | 6 | 2.2 | 195 | 9  | Q8W740 | Q8w740 bacterioph   | 895 | 6 | 2.2 | 219 | 10 | Q9LQ01  | Q9lq01 oryza sativ  |
| 823 | 6 | 2.2 | 195 | 16 | Q9C195 | Q9c195 lactococcus  | 896 | 6 | 2.2 | 219 | 17 | Q9YE48  | Q9ye48 aeropyrum p  |
| 824 | 6 | 2.2 | 195 | 16 | Q8XYI8 | Q8xyi8 ralstonia s  | 897 | 6 | 2.2 | 219 | 17 | Q8ULX9  | Q8ulx9 pyrococcus   |
| 825 | 6 | 2.2 | 195 | 16 | Q9RDB2 | Q9rdb2 streptomyce  | 898 | 6 | 2.2 | 220 | 11 | Q9CY73  | Q9cy73 mus musculu  |
| 826 | 6 | 2.2 | 195 | 17 | Q97W11 | Q97w11 sulfolobus   | 899 | 6 | 2.2 | 220 | 16 | Q8WXY0  | Q8wxy0 thermotoga   |
| 827 | 6 | 2.2 | 196 | 9  | Q9AZE1 | Q9aze1 bacterioph   | 900 | 6 | 2.2 | 220 | 16 | Q8NSQ0  | Q8nsg0 corynebacte  |
| 828 | 6 | 2.2 | 196 | 16 | Q9K7G5 | Q9k7g5 bacillus ha  | 901 | 6 | 2.2 | 220 | 17 | Q9HQA1  | Q9hqa1 halobacteri  |
| 829 | 6 | 2.2 | 196 | 16 | Q9C145 | Q9c145 lactococcus  | 902 | 6 | 2.2 | 221 | 9  | Q8M6Z3  | Q8m6z3 cyanophage   |
| 830 | 6 | 2.2 | 197 | 11 | Q99LE1 | Q99le1 mus musculu  | 903 | 6 | 2.2 | 221 | 11 | Q99NT6  | Q99nt6 cavia tachu  |
| 831 | 6 | 2.2 | 198 | 16 | Q98ME5 | Q98me5 rhizobium l  | 904 | 6 | 2.2 | 221 | 16 | Q8F3U8  | Q8f3u8 leptospira   |
| 832 | 6 | 2.2 | 199 | 2  | Q93F24 | Q93f24 pectobacter  | 905 | 6 | 2.2 | 222 | 10 | Q42458  | Q42458 arabidopsis  |
| 833 | 6 | 2.2 | 199 | 16 | Q8DCR9 | Q8dcr9 vibrio vuln  | 906 | 6 | 2.2 | 222 | 16 | Q8XM50  | Q8xm50 clostridium  |
| 834 | 6 | 2.2 | 200 | 2  | Q53660 | Q53660 staphylococ  | 907 | 6 | 2.2 | 223 | 8  | Q8MLN1  | Q8mln1 minioterus   |
| 835 | 6 | 2.2 | 200 | 5  | Q8SRF8 | Q8srf8 encephalito  | 908 | 6 | 2.2 | 223 | 17 | Q979V1  | Q979v1 thermoplasm  |
| 836 | 6 | 2.2 | 200 | 16 | Q8ZCY8 | Q8zcy8 yersinia pe  | 909 | 6 | 2.2 | 224 | 5  | Q9TXY5  | Q9txy5 caenorhabdi  |
| 837 | 6 | 2.2 | 201 | 2  | Q87962 | Q87962 streptomyce  | 910 | 6 | 2.2 | 224 | 10 | Q9FHW4  | Q9fhw4 arabidopsis  |
| 838 | 6 | 2.2 | 201 | 10 | Q9FEY4 | Q9fey4 heterocapsa  | 911 | 6 | 2.2 | 224 | 16 | Q914Z2  | Q914z2 pseudomonas  |
| 839 | 6 | 2.2 | 201 | 16 | Q9PQ92 | Q9pq92 ureaplasma   | 912 | 6 | 2.2 | 224 | 17 | Q97B88  | Q97b88 thermoplasm  |
| 840 | 6 | 2.2 | 201 | 16 | Q9KNX6 | Q9knx6 vibrio chol  | 913 | 6 | 2.2 | 225 | 5  | Q9V5R7  | Q9v5r7 drosophila   |
| 841 | 6 | 2.2 | 201 | 16 | Q8ZE22 | Q8ze22 yersinia pe  | 914 | 6 | 2.2 | 225 | 5  | P91673  | P91673 drosophila   |
| 842 | 6 | 2.2 | 202 | 4  | Q96F40 | Q96f40 homo sapien  | 915 | 6 | 2.2 | 225 | 17 | Q9HSR5  | Q9hsr5 halobacteri  |
| 843 | 6 | 2.2 | 202 | 4  | Q96L06 | Q96lq6 homo sapien  | 916 | 6 | 2.2 | 226 | 5  | Q8IU23  | Q8iut3 brachiosteo  |
| 844 | 6 | 2.2 | 202 | 8  | Q21015 | Q21015 choanophal   | 917 | 6 | 2.2 | 226 | 8  | Q8LYF7  | Q8lyf7 chauiognat   |
| 845 | 6 | 2.2 | 202 | 10 | Q949E8 | Q949e8 oryza sativ  | 918 | 6 | 2.2 | 226 | 16 | Q9RRJ9  | Q9rrj9 deinococcus  |
| 846 | 6 | 2.2 | 202 | 16 | Q8D0L3 | Q8d0l3 yersinia pe  | 919 | 6 | 2.2 | 227 | 16 | Q983J3  | Q983j3 rhizobium l  |
| 847 | 6 | 2.2 | 203 | 5  | Q95YV3 | Q95ym3 nipostrong   | 920 | 6 | 2.2 | 228 | 2  | P77131  | P77131 escherichia  |
| 848 | 6 | 2.2 | 203 | 8  | Q21009 | Q21009 choanophal   | 921 | 6 | 2.2 | 228 | 10 | Q94FQ9  | Q94fq9 arabidopsis  |
| 849 | 6 | 2.2 | 203 | 16 | Q8F6L2 | Q8f6l2 leptospira   | 922 | 6 | 2.2 | 228 | 10 | Q9LYI0  | Q9lyi0 arabidopsis  |
| 850 | 6 | 2.2 | 204 | 2  | Q8D6L8 | Q8d6l8 vibrio vuln  | 923 | 6 | 2.2 | 228 | 10 | Q8GM01  | Q8gm01 oryza sativ  |
| 851 | 6 | 2.2 | 204 | 2  | Q9R3D8 | Q9r3d8 pseudomonas  | 924 | 6 | 2.2 | 228 | 16 | Q9RWL7  | Q9rw17 deinococcus  |
| 852 | 6 | 2.2 | 204 | 2  | Q9R308 | Q9r308 pseudomonas  | 925 | 6 | 2.2 | 228 | 16 | Q8PL44  | Q8pl44 xanthomonas  |
| 853 | 6 | 2.2 | 204 | 2  | Q9WJ00 | Q9wj00 pseudomonas  | 926 | 6 | 2.2 | 228 | 16 | Q8FK46  | Q8fk46 escherichia  |
| 854 | 6 | 2.2 | 204 | 2  | Q9R307 | Q9r307 pseudomonas  | 927 | 6 | 2.2 | 229 | 11 | Q91W91  | Q91w91 mus musculu  |
| 855 | 6 | 2.2 | 204 | 2  | Q9R347 | Q9r347 pseudomonas  | 928 | 6 | 2.2 | 229 | 12 | Q9WHT9  | Q9wht9 bluetongue   |
| 856 | 6 | 2.2 | 204 | 2  | Q9WJ19 | Q9wj19 pseudomonas  | 929 | 6 | 2.2 | 229 | 16 | Q9AAG0  | Q9aag0 caulobacter  |
| 857 | 6 | 2.2 | 204 | 2  | Q9RBY4 | Q9rby4 pseudomonas  | 930 | 6 | 2.2 | 229 | 16 | Q97EG6  | Q97eg6 clostridium  |
| 858 | 6 | 2.2 | 204 | 2  | Q9R3D6 | Q9r3d6 pseudomonas  | 931 | 6 | 2.2 | 229 | 16 | Q8VEJ6  | Q8vej6 bruceella me |
| 859 | 6 | 2.2 | 204 | 2  | Q9R436 | Q9r436 pseudomonas  | 932 | 6 | 2.2 | 229 | 16 | Q8G387  | Q8g387 bruceella su |
| 860 | 6 | 2.2 | 204 | 2  | Q9R272 | Q9r272 pseudomonas  | 933 | 6 | 2.2 | 229 | 17 | Q9HK08  | Q9hk08 thermoplasm  |
| 861 | 6 | 2.2 | 204 | 2  | Q9R9F3 | Q9r9f3 pseudomonas  | 934 | 6 | 2.2 | 230 | 5  | Q9V5B7  | Q9v5b7 drosophila   |
| 862 | 6 | 2.2 | 204 | 2  | Q9R3D7 | Q9r3d7 pseudomonas  | 935 | 6 | 2.2 | 230 | 16 | Q8E2V7  | Q8e2v7 streptococc  |
| 863 | 6 | 2.2 | 206 | 2  | Q9RNL0 | Q9rnl0 yzomonas m   | 936 | 6 | 2.2 | 230 | 16 | Q8DX08  | Q8dx08 streptococc  |
| 864 | 6 | 2.2 | 206 | 5  | Q95SUL | Q95sul drosophila   | 937 | 6 | 2.2 | 231 | 2  | Q8KX12  | Q8kx12 synechococc  |
| 865 | 6 | 2.2 | 206 | 11 | Q9EPQ4 | Q9epq4 mus musculu  | 938 | 6 | 2.2 | 231 | 12 | Q9J968  | Q9j968 propouche v  |
| 866 | 6 | 2.2 | 206 | 11 | Q8CDE3 | Q8cde3 mus musculu  | 939 | 6 | 2.2 | 231 | 16 | Q8R7U3  | Q8r7u3 thermomae    |
| 867 | 6 | 2.2 | 206 | 16 | Q916A6 | Q916a6 pseudomonas  | 940 | 6 | 2.2 | 231 | 16 | Q8F9B1  | Q8f9b1 leptospira   |
| 868 | 6 | 2.2 | 207 | 11 | Q9QYI3 | Q9qyi3 mus musculu  | 941 | 6 | 2.2 | 232 | 5  | Q9V5B4  | Q9v5b4 drosophila   |
| 869 | 6 | 2.2 | 208 | 5  | Q95VX8 | Q95vx8 trypanosoma  | 942 | 6 | 2.2 | 232 | 11 | Q8R345  | Q8r345 mus musculu  |
| 870 | 6 | 2.2 | 208 | 11 | Q9D3U7 | Q9d3u7 mus musculu  | 943 | 6 | 2.2 | 232 | 16 | Q8DVS9  | Q8dva9 streptococc  |
| 871 | 6 | 2.2 | 209 | 16 | Q8NXU9 | Q8nxu9 staphylococ  | 944 | 6 | 2.2 | 233 | 12 | Q98J11  | Q98j11 molluscum c  |
| 872 | 6 | 2.2 | 210 | 5  | Q8SUR0 | Q8sufo encephalito  | 945 | 6 | 2.2 | 233 | 16 | Q9YEZ9  | Q9yez9 bruceella me |
| 873 | 6 | 2.2 | 211 | 1  | Q977R7 | Q977r7 uncultured   | 946 | 6 | 2.2 | 234 | 8  | Q95F64  | Q95f64 eimeria sep  |
| 874 | 6 | 2.2 | 211 | 3  | Q9C4R3 | Q9c4r3 methanococc  | 947 | 6 | 2.2 | 234 | 17 | Q9HQX0  | Q9hqx0 halobacteri  |
| 875 | 6 | 2.2 | 211 | 3  | Q90026 | Q90026 ajiellomyces | 948 | 6 | 2.2 | 235 | 16 | Q92WQ2  | Q92wg2 rhizobium m  |
| 876 | 6 | 2.2 | 211 | 4  | Q969X0 | Q969x0 homo sapien  | 949 | 6 | 2.2 | 236 | 10 | Q9LR02  | Q9lr02 arabidopsis  |
| 877 | 6 | 2.2 | 211 | 16 | Q8VKC3 | Q8vkc3 mycobacteri  | 950 | 6 | 2.2 | 236 | 13 | Q9YHW7  | Q9yhw7 gallus gall  |
| 878 | 6 | 2.2 | 212 | 5  | Q8MPAL | Q8mpal dictyosteli  | 951 | 6 | 2.2 | 236 | 17 | Q97ZX2  | Q97zx2 sulfolobus   |
| 879 | 6 | 2.2 | 212 | 8  | Q9T5A5 | Q9t5a5 solanum tub  | 952 | 6 | 2.2 | 238 | 10 | Q9GVJ5  | Q9gvj5 oryza sativ  |
| 880 | 6 | 2.2 | 213 | 10 | Q948D7 | Q948d7 oryza sativ  | 953 | 6 | 2.2 | 238 | 11 | Q99JUR7 | Q99jr7 mus musculu  |
| 881 | 6 | 2.2 | 213 | 11 | Q9CSB4 | Q9csb4 mus musculu  | 954 | 6 | 2.2 | 238 | 17 | Q59452  | Q59452 pyrococcus   |
| 882 | 6 | 2.2 | 214 | 16 | Q98SE9 | Q98se9 rhizobium l  | 955 | 6 | 2.2 | 238 | 17 | Q8ZVE9  | Q8zve9 pyrobaculum  |
| 883 | 6 | 2.2 | 214 | 17 | Q97A59 | Q97a59 thermoplasm  | 956 | 6 | 2.2 | 239 | 4  | Q9BPV9  | Q9bpv9 homo sapien  |
| 884 | 6 | 2.2 | 215 | 5  | Q8ITG9 | Q8itg9 biomphalari  | 957 | 6 | 2.2 | 239 | 4  | Q96SS6  | Q96s66 homo sapien  |
| 885 | 6 | 2.2 | 215 | 16 | Q92WN5 | Q92wn5 rhizobium m  | 958 | 6 | 2.2 | 239 | 4  | Q9UKD2  | Q9ukd2 homo sapien  |
| 886 | 6 | 2.2 | 215 | 16 | Q9L0F0 | Q9l0f0 streptomyce  | 959 | 6 | 2.2 | 239 | 10 | Q9FTA2  | Q9fta2 arabidopsis  |
| 887 | 6 | 2.2 | 216 | 1  | Q9C4R2 | Q9c4r2 methanococc  | 960 | 6 | 2.2 | 239 | 11 | Q9D0I8  | Q9d0i8 mus musculu  |
| 888 | 6 | 2.2 | 216 | 1  | Q9C4Q0 | Q9c4q0 methanococc  | 961 | 6 | 2.2 | 239 | 11 | Q8CS91  | Q8cs91 mus musculu  |
| 889 | 6 | 2.2 | 216 | 10 | Q94FQ1 | Q94fq1 arabidopsis  | 962 | 6 | 2.2 | 239 | 16 | Q988Q3  | Q988q3 rhizobium l  |
| 890 | 6 | 2.2 | 216 | 10 | Q93W13 | Q93w13 arabidopsis  | 963 | 6 | 2.2 | 239 | 16 | Q92J89  | Q92j89 rickettsia   |
| 891 | 6 | 2.2 | 216 | 16 | Q98FF4 | Q98ff4 rhizobium l  | 964 | 6 | 2.2 | 240 | 2  | O68993  | O68993 chlorobium   |
| 892 | 6 | 2.2 | 217 | 10 | Q9LP12 | Q9lp12 arabidopsis  | 965 | 6 | 2.2 | 240 | 16 | Q8G851  | Q8g851 bifidobacte  |

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966 6 2.2 240 16 Q8DP95 Q8dp95 streptococc
967 6 2.2 241 2 P94219 borrellia af
968 6 2.2 241 5 Q8LGD2 Q8lgd2 drosophila
969 6 2.2 241 10 Q9LFP2 Q9lfp2 arabidopsis
970 6 2.2 241 10 Q84674 Q84674 paramescion
971 6 2.2 241 16 Q8XU43 Q8xu43 ralstonia s
972 6 2.2 242 2 Q9EXK6 Q9exk6 streptomyc
973 6 2.2 242 16 Q9KBR6 Q9kbr6 bacillus ha
974 6 2.2 242 16 Q9CLG8 Q9clg8 pasteurilla
975 6 2.2 242 16 Q8ZKK9 Q8zkk9 salmonella
976 6 2.2 242 16 Q9CEG9 Q9ceg9 lactococcus
977 6 2.2 243 16 Q8K90 Q8k90 rhizobium l
978 6 2.2 243 16 Q8ZM56 Q8zm56 salmonella
979 6 2.2 243 16 Q8PLH4 Q8plh4 xanthomonas
980 6 2.2 244 3 Q06760 Q06760 saccharomyc
981 6 2.2 244 3 Q03888 Q03888 saccharomyc
982 6 2.2 244 10 Q8H805 Q8hus5 oryza sativ
983 6 2.2 244 16 Q8R249 Q8r249 deinococcus
984 6 2.2 244 16 Q99Y06 Q99yd6 streptococc
985 6 2.2 244 16 Q97Q07 Q97q07 streptococc
986 6 2.2 244 16 Q8ZQV6 Q8zqv6 salmonella
987 6 2.2 244 16 Q8Z8D9 Q8z8d9 salmonella
988 6 2.2 244 16 Q8X9C8 Q8x9c8 escherichia
989 6 2.2 244 16 Q8X815 Q8x815 escherichia
990 6 2.2 244 16 Q8NZN2 Q8nzn2 streptococc
991 6 2.2 244 16 Q8K628 Q8k628 streptococc
992 6 2.2 244 16 Q8ZF75 Q8zft5 versinia pe
993 6 2.2 244 16 Q8FJU6 Q8fju6 escherichia
994 6 2.2 244 16 Q8ETD2 Q8etd2 oceanobacil
995 6 2.2 244 16 Q8EAW5 Q8eaw5 shewanella
996 6 2.2 244 16 Q8D5NS Q8dan5 streptococc
997 6 2.2 245 4 Q9NRX8 Q9nrx8 homo sapien
998 6 2.2 245 4 Q9RUT1 Q9rut1 homo sapien
999 6 2.2 245 7 Q31591 Q31591 salmo salar
1000 6 2.2 245 8 Q8MOC9 Q8moc9 amosibidium
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## ALIGNMENTS

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RESULT 1
Q94KL7 ID Q94KL7 PRELIMINARY; PRT; 277 AA.
AC Q94KL7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Stem secoisolariciresinol dehydrogenase (Fragment).
OS Forsythia intermedia (Border forsythia).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridaceae; Lamiids; Solanales; Oleaceae; Forsythia.
OX NCBI_TaxID=55183;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21201084; PubMed=11278426;
RA Xia Z.Q.; Costa M.A.; Pelissier H.C.; Davin L.B.; Lewis N.G.;
RT "Secoisolariciresinol dehydrogenase Purification, Cloning, and
RT Functional Expression. IMPLICATIONS FOR HUMAN HEALTH PROTECTION."
RL J. Biol. Chem. 276:12614-12623(2001).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AF352735; AAK38665.1; --
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase.
FT NON TER 277
SQ SEQUENCE 277 AA; 29256 MW; 98885C210CAFE2EB CRC64;

Query Match 40.3%; Score 110; DB 10; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.3e-110;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
Q40590 ID Q40590 PRELIMINARY; PRT; 234 AA.
AC Q40590;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE THP-1 protein.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridaceae; Lamiids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Petite Havana SR-1;
RX MEDLINE=95004656; PubMed=7920706;
RA Kawaoka A.; Kawamoto T.; Sekine M.; Yoshida K.; Takano M.; Shinmyo A.;
RT "A cis-acting element and a trans-acting factor involved in the wound-
RT induced expression of a horseradish peroxidase gene.";
RL Plant J. 6:87-97(1994).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; D29976; BAA06241.1; --
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
KW Oxidoreductase.
SQ SEQUENCE 234 AA; 25078 MW; F10BD4E0FF97940A CRC64;

Query Match 6.2%; Score 17; DB 10; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 RLEGKVALITGGASGIG 26
DB 13 RLEGKVALITGGASGIG 29

RESULT 3
O50038 ID O50038 PRELIMINARY; PRT; 284 AA.
AC O50038;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Short chain alcohol dehydrogenase.
GN SCANT.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridaceae; Lamiids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Leaf;
RC Moenke G.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=96145513; PubMed=8555446;
RA Herbers K.; Moenke G.; Badur R.; Sonnenwald U.;
```

RT "A simplified procedure for the subtractive cDNA cloning of  
 RT photoassimilate-responding genes: isolation of cDNAs encoding a new  
 RT class of pathogenesis-related proteins.";  
 RL Plant Mol. Biol. 29:1027-1038(1995).  
 CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.

DR EMBL; AJ223178; CAA11154.1; -.  
 DR EMBL; AJ223177; CAA11153.1; -.  
 DR HSSP; P19992; IHDC.  
 DR InterPro; IPR002198; ADH short.  
 DR Pfam; PF00106; adh\_short; 1.  
 DR PRINTS; PR00080; SDRFAMILY.  
 DR PROSITE; PS00061; ADH\_SHORT; 1.  
 KW Oxidoreductase.  
 SQ SEQUENCE 284 AA; 29819 MW; BD884E9013FB63E9 CRC64;

Query Match 6.2%; Score 17; DB 10; Length 284;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-09;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 RLEGKVALITGASGIG 26  
 Db 13 RLEGKVALITGASGIG 29  
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RESULT 4  
 Q9ZR17 PRELIMINARY; PRT; 283 AA.

AC Q9ZR17;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Putative alcohol dehydrogenase.  
 GN F4C21.6 OR At4G03140.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Habermann K., de la Bastide M., Huang E.N., Gnoj L., Schutz K.,  
 RA Preston R., Calma C., Martienssen R., Parnell L.D., Dedhia N.,  
 RA McCombie W.R.;  
 RA "Arabidopsis thaliana BAC F4C21 from chromosome IV near 17 cm.";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M.,  
 RA Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M.,  
 RA Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N.,  
 RA Mewes H.W., Lemcke K., Mayer K.F.X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
 DR EMBL; AC005275; AAD14442.1; -.  
 DR EMBL; AL161496; CAB7799.1; -.  
 DR HSSP; P19992; IHDC.  
 DR InterPro; IPR002198; ADH short.  
 DR Pfam; PF00106; adh\_short; 1.  
 DR PRINTS; PR00080; SDRFAMILY.  
 DR PROSITE; PS00061; ADH\_SHORT; 1.  
 KW Oxidoreductase.

SQ SEQUENCE 283 AA; 29994 MW; 93B0A97CECC859BC CRC64;  
 Query Match 5.9%; Score 16; DB 10; Length 283;  
 Best Local Similarity 100.0%; Pred. No. 2e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LEGKVALITGASGIG 26  
 Db 18 LEGKVALITGASGIG 33  
 |||||

RESULT 5  
 Q941B4 PRELIMINARY; PRT; 306 AA.

AC Q941B4;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE AT3g26770/MDJ14\_21.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,  
 RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayaehizaki Y.,  
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,  
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,  
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,  
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,  
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,  
 RA Ecker J.R.;  
 RA "Arabidopsis cDNA clones";  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
 DR EMBL; AY052216; AAK97686.1; -.  
 DR InterPro; IPR002198; ADH\_short.  
 DR Pfam; PF00106; adh\_short; 1.  
 DR PRINTS; PR00080; SDRFAMILY.  
 KW Oxidoreductase.  
 SQ SEQUENCE 306 AA; 31795 MW; C1816892BF71B537 CRC64;

Query Match 5.1%; Score 14; DB 10; Length 306;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LEGKVALITGASG 24  
 Db 41 LEGKVALITGASG 54  
 |||||

RESULT 6  
 Q9LW34 PRELIMINARY; PRT; 306 AA.

ID Q9LW34;  
 AC Q9LW34;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Alcohol dehydrogenase-like protein (At3g26770/MDJ14\_21).  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Columbia;  
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;  
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Columbia;  
 RX MEDLINE=20277480; PubMed=10819329;  
 RA Nakamura Y.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence  
 features of the regions of 4,504,864 bp covered by sixty P1 and TAC

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RESULT 8
Q8HOD9 Q8HOD9 PRELIMINARY; PRT; 274 AA.
ID Q8HOD9;
AC AC Q8HOD9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ADH Alcohol dehydroge.
GN ADH.
OS Os Phaseolus lunatus (Lima bean) (Phaseolus limensis).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
NCBI_TaxID=3984;
RN [1]
RX RX
UN UN
RP RP SEQUENCE FROM N.A.
RA Horiuchi J., Arimura G., Ozawa R., Muroi A., Takabayashi J.,
RA Nishioka T.;
RT "Phaseolus lunatus.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RD EMBL; AB086038; BACS3872.1; -.
SQ SEQUENCE 274 AA; 28862 MW; DEC85BDB324877F CRC64;

Query Match 4.8%; Score 13; DB 10; Length 274;
Best Local Similarity 100.0%; Pred. No. 3.5e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 AVELGQFGIRVNC 189
DB 178 AVELGQFGIRVNC 190

RESULT 9
Q8LID4 Q8LID4 PRELIMINARY; PRT; 321 AA.
ID Q8LID4;
AC AC Q8LID4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE OJ1343 D04.14 protein (P0453E03.33 protein).
DE OJ1343 D04.14 OR P0453E03.33.
DE Oryza sativa (japonica cultivar-group).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartioideae; Oryzeae; Oryza.
NCBI_TaxID=39947;
RN [1]
RX RX
UN UN SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
DE "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC
clone:OJ1343 D04.",
DE Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Katayose Y.;
DE "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC
clone:P0453E03.",
DE Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
-1- SIMILARITY (JUN-2002) TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
EMBL; AP003825; BAC10093.1; -.
EMBL; AP005452; BAC22441.1; -.
Gramine; Q8LID4; -.
InterPro; IPR002198; ADH short.
pfam; PF00106; adh_short; 1.
PRINTS; PR00080; SDRFAMILY.
Oxidoreductase.
SQ SEQUENCE 321 AA; 34337 MW; 3DB5EC4726D98AA2 CRC64;

Query Match 4.8%; Score 13; DB 10; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 235 AALYLASDEAKV 247  
 Db 287 AALYLASDEAKV 299

RESULT 10

Q8S9B7 PRELIMINARY; PRT; 160 AA.

AC Q8S9B7;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE S-locus linked stigma protein 1 (Fragment).  
 GN SSPI.  
 OS Ipomoea trifida.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamids; Solanales; Convolvulaceae; Ipomoea.  
 OX NCBI\_TaxID=35884;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H45-3;  
 RA Tsuchiya T., Suwabe K., Watase T., Kagaya Y., Koyama Y.;  
 RT "Characterization of promoter region of the SSP gene from Ipomoea  
 trifida regulates stigma-specific expression."  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
 CC  
 DR EMBL; AB070220; BAB86915.1;  
 DR InterPro; IPR002198; ADH\_short.  
 DR Pfam; PF00106; adh\_short; 1.  
 DR Oxidoreductase.  
 DR NON TER 160  
 FT SEQUENCE 160 AA; 16817 MW; BABBF82727F12694 CRC64;  
 SQ

Query Match 4.4%; Score 12; DB 10; Length 160;  
 Best Local Similarity 100.0%; Pred. No. 0.00026;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 86 YGKLDIMFSNAG 97  
 Db 89 YGKLDIMFSNAG 100

RESULT 11

Q8SBD7 PRELIMINARY; PRT; 277 AA.

AC Q8SBD7;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Short-chain alcohol dehydrogenase (S-locus linked stigma  
 protein).  
 GN SSP OR SSP10.  
 OS Ipomoea trifida.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamids; Solanales; Convolvulaceae; Ipomoea.  
 OX NCBI\_TaxID=35884;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Koyama Y., Kadota N., Sassa H., Kakeda K., Tsuchiya T., Ishimizu T.,  
 RA Kondo K., Norioka S.;  
 RT "S-locus specific stigma protein (SSP) from sporophytic self-  
 incompatibility plant, Ipomoea trifida, is a member of short-chain  
 alcohol dehydrogenase family."  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H77-2;  
 RA Tsuchiya T., Suwabe K., Watase T., Kagaya Y., Koyama Y.;

RT "Characterization of promoter region of the SSP gene from Ipomoea  
 trifida regulates stigma-specific expression."  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
 CC  
 DR EMBL; AF072449; AAC35342.1;  
 DR EMBL; AB070221; BAB86916.1;  
 DR HSSP; P19992; IHDC.  
 DR InterPro; IPR002198; ADH\_short.  
 DR Pfam; PF00106; adh\_short; 1.  
 DR PRINTS; PR00080; SDRFAMILY.  
 DR Oxidoreductase.  
 KW SEQUENCE 277 AA; 29257 MW; AOCDB434B31C666D CRC64;  
 SQ

Query Match 4.4%; Score 12; DB 10; Length 277;  
 Best Local Similarity 100.0%; Pred. No. 0.00043;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 86 YGKLDIMFSNAG 97  
 Db 89 YGKLDIMFSNAG 100

RESULT 12

Q8SBD8 PRELIMINARY; PRT; 277 AA.

AC Q8SBD8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Short-chain alcohol dehydrogenase.  
 GN SSP.  
 OS Ipomoea trifida.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamids; Solanales; Convolvulaceae; Ipomoea.  
 OX NCBI\_TaxID=35884;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Koyama Y., Kadota N., Sassa H., Kakeda K., Tsuchiya T., Ishimizu T.,  
 RA Kondo K., Norioka S.;  
 RT "S-locus specific stigma protein (SSP) from sporophytic self-  
 incompatibility plant, Ipomoea trifida, is a member of short-chain  
 alcohol dehydrogenase family."  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
 CC  
 DR EMBL; AF072448; AAC35341.1;  
 DR HSSP; P19992; IHDC.  
 DR InterPro; IPR002198; ADH\_short.  
 DR Pfam; PF00106; adh\_short; 1.  
 DR PRINTS; PR00080; SDRFAMILY.  
 DR Oxidoreductase.  
 KW SEQUENCE 277 AA; 29312 MW; 7A75BEF12A73D9AE CRC64;  
 SQ

Query Match 4.4%; Score 12; DB 10; Length 277;  
 Best Local Similarity 100.0%; Pred. No. 0.00043;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 86 YGKLDIMFSNAG 97  
 Db 89 YGKLDIMFSNAG 100

RESULT 13

Q8SBD6 PRELIMINARY; PRT; 284 AA.

AC Q8SBD6;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Short-chain alcohol dehydrogenase.  
 GN SSP.

```
OS Ipomoea trifida.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Convolvulaceae; Ipomoea.
OX NCBI_TaxID=35884;
EN [1]
RP SEQUENCE FROM N.A.
RA Koyama Y., Kadota N., Sassa H., Kakeda K., Tsuchiya T., Ishimizu T.,
RA Kondo K., Norioka S.;
RT S-locus specific stigma protein (SSP) from sporophytic self-
RT incompatibility plant, Ipomoea trifida, is a member of short-chain
RT alcohol dehydrogenase family."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AF072450; AAC35343.1; -.
DR HSSP; P19992; IHDC.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR OXidoreductase.
KW OXidoreductase.
SQ SEQUENCE 284 AA; 29898 MW; 2B54BFFBAD6BAE4A CRC64;

Query Match 4.4%; Score 12; DB 10; Length 284;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 86 YGKLDIMFSNAG 97
Db 89 YGKLDIMFSNAG 100

RESULT 14
O82465 PRELIMINARY; PRT; 284 AA.
ID O82465;
AC O82465;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Short-chain alcohol dehydrogenase.
GN SSP.
OS Ipomoea trifida.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Convolvulaceae; Ipomoea.
OX NCBI_TaxID=35884;
EN [1]
RP SEQUENCE FROM N.A.
RA Koyama Y., Kadota N., Sassa H., Kakeda K., Tsuchiya T., Ishimizu T.,
RA Kondo K., Norioka S.;
RT S-locus specific stigma protein (SSP) from sporophytic self-
RT incompatibility plant, Ipomoea trifida, is a member of short-chain
RT alcohol dehydrogenase family."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AF072447; AAC35340.1; -.
DR HSSP; P19992; IHDC.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR OXidoreductase.
KW OXidoreductase.
SQ SEQUENCE 284 AA; 29823 MW; 4C04A888178C0633 CRC64;

Query Match 4.4%; Score 12; DB 10; Length 284;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 86 YGKLDIMFSNAG 97
Db 89 YGKLDIMFSNAG 100
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RESULT 15
P87017 PRELIMINARY; PRT; 278 AA.
ID P87017;
AC P87017;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Short-chain alcohol dehydrogenase.
GN ADHA.
OS Aspergillus parasiticus.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic trichocomaceae; Aspergillus.
OX NCBI_TaxID=5067;
EN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=SU-1;
RX MEDLINE=20509789; PubMed=11055914;
RA Chang P.K., Yu J., Ehrlich K.C., Boue S.M., Montalbano B.G.,
RA Bhatnagar D., Cleveland T.E.;
RT "adha in Aspergillus parasiticus Is Involved in Conversion of 5'-
RT Hydroxyaverrantin to Averufin."
RL Appl. Environ. Microbiol. 66:4715-4719(2000).
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; U76621; AAB51228.3; -.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW OXidoreductase.
SQ SEQUENCE 278 AA; 29557 MW; 8C60C5437EB9BB71 CRC64;

Query Match 4.0%; Score 11; DB 3; Length 278;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ALITGGASGIG 26
Db 18 ALITGGASGIG 28

Search completed: October 23, 2003, 13:05:29
Job time : 163 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 23, 2003, 12:37:54 ; Search time 85 Seconds  
(without alignments)  
509.792 Million cell updates/sec

Title: US-09-673-918A-2

Perfect score: 1393

Sequence: 1 MQLRTAFARLEKGVALTG.....IDGFSVCNSVIKVFQVPS 273

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_19Jun03;\*

- 1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*
- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
- 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*
- 5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*
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- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description                 |
|------------|-------|-------------|--------|----|-----------------------------|
| 1          | 1393  | 100.0       | 273    | 21 | AA54412 Secoisolariciresin  |
| 2          | 1388  | 99.6        | 272    | 21 | AA54420 Secoisolariciresin  |
| 3          | 1364  | 97.9        | 277    | 21 | AA54413 Secoisolariciresin  |
| 4          | 1233  | 88.5        | 276    | 21 | AA54416 Secoisolariciresin  |
| 5          | 1233  | 88.5        | 276    | 23 | AA021494 Secoisolariciresin |
| 6          | 1223  | 87.8        | 273    | 21 | AA54414 Secoisolariciresin  |
| 7          | 1175  | 84.4        | 277    | 21 | AA54415 Secoisolariciresin  |
| 8          | 658.5 | 47.3        | 285    | 23 | ABB91329 Herbicidally activ |
| 9          | 654.5 | 47.0        | 285    | 21 | AAG25524 Arabidopsis thalia |

|    |       |      |     |    |          |                     |
|----|-------|------|-----|----|----------|---------------------|
| 10 | 625.5 | 44.9 | 303 | 23 | ABB92624 | Herbicidally activ  |
| 11 | 598.5 | 43.0 | 300 | 21 | AAG18620 | Arabidopsis thalia  |
| 12 | 598.5 | 43.0 | 343 | 21 | AAG18619 | Arabidopsis thalia  |
| 13 | 597.5 | 42.9 | 283 | 21 | AAG31552 | Arabidopsis thalia  |
| 14 | 597.5 | 42.9 | 283 | 23 | ABB92823 | Herbicidally activ  |
| 15 | 588.5 | 42.2 | 336 | 16 | AAW06488 | Maize Tst2 sequence |
| 16 | 588   | 42.2 | 289 | 23 | ABB92448 | Herbicidally activ  |
| 17 | 578.5 | 41.5 | 261 | 21 | AAG24387 | Arabidopsis thalia  |
| 18 | 578.5 | 41.5 | 276 | 21 | AAG24386 | Arabidopsis thalia  |
| 19 | 575.5 | 41.3 | 264 | 23 | ABB92145 | Herbicidally activ  |
| 20 | 575.5 | 41.3 | 274 | 21 | AAG51580 | Arabidopsis thalia  |
| 21 | 573.5 | 41.2 | 260 | 21 | AAG51581 | Arabidopsis thalia  |
| 22 | 573.5 | 41.2 | 260 | 23 | ABB92475 | Herbicidally activ  |
| 23 | 569   | 40.8 | 280 | 23 | ABB92449 | Herbicidally activ  |
| 24 | 568.5 | 40.8 | 286 | 21 | AAG51575 | Arabidopsis thalia  |
| 25 | 567   | 40.7 | 257 | 21 | AAG31795 | Herbicidally activ  |
| 26 | 567   | 40.7 | 257 | 23 | ABB92144 | Herbicidally activ  |
| 27 | 566   | 40.6 | 259 | 23 | ABB92476 | Herbicidally activ  |
| 28 | 565   | 40.6 | 257 | 21 | AAG51577 | Arabidopsis thalia  |
| 29 | 549.5 | 39.4 | 258 | 23 | ABB92143 | Herbicidally activ  |
| 30 | 492.5 | 35.4 | 272 | 21 | AAG09589 | Arabidopsis thalia  |
| 31 | 492.5 | 35.4 | 275 | 21 | AAG09588 | Arabidopsis thalia  |
| 32 | 490.5 | 35.2 | 272 | 23 | ABB92500 | Herbicidally activ  |
| 33 | 487.5 | 35.0 | 272 | 21 | AAU77928 | A. thaliana enviro  |
| 34 | 432   | 31.0 | 253 | 22 | AAU36249 | Pseudomonas aerugi  |
| 35 | 403.5 | 29.0 | 159 | 21 | AAG25525 | Arabidopsis thalia  |
| 36 | 375.5 | 27.0 | 146 | 21 | AAG25526 | Arabidopsis thalia  |
| 37 | 370   | 26.6 | 186 | 21 | AAG18621 | Arabidopsis thalia  |
| 38 | 370   | 26.6 | 186 | 21 | AAG31553 | Arabidopsis thalia  |
| 39 | 370   | 26.6 | 186 | 21 | AAG38248 | Arabidopsis thalia  |
| 40 | 363   | 26.1 | 254 | 23 | ABB48207 | Listeria monocytog  |
| 41 | 357   | 25.6 | 251 | 20 | AAU34891 | Chlamydia pneumoni  |
| 42 | 349.5 | 25.1 | 262 | 22 | AA886337 | G. suboxydans DSM   |
| 43 | 347.5 | 24.9 | 262 | 21 | AAV44578 | Xylitol dehydrogen  |
| 44 | 346.5 | 24.9 | 253 | 23 | ABB50010 | Listeria monocytog  |
| 45 | 343.5 | 24.7 | 267 | 22 | AA847459 | Levodione reductas  |

#### ALIGNMENTS

#### RESULT 1

AA54412

ID AAY54412 standard; Protein; 273 AA.

XX AC AAY54412;

XX AC AAY54412;

XX DT 06-APR-2000 (first entry)

XX DE Secoisolariciresinol dehydrogenase protein clone DEHY133.

XX DE Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway;

XX KW lignan; matiarensinol; health-protecting lignan; phytoestrogen;

XX KW enterolactone; enterodiol; neutriceutical; dietary supplement;

XX KW (-)-trachelogenin; antiviral; (-)-podophyllotoxin.

XX OS Forsythia intermedia.

XX XX

XX PN WO9955846-A1.

XX PD 04-NOV-1999.

XX PF 23-APR-1999; 99WO-US08975.

XX XX

XX XX 24-APR-1998; 98US-0082977.

XX PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.

XX XX

XX PI Xia Z, Costa MA, Davin LB, Lewis NG;

XX XX

XX DR WPI; 2000-136356/11.

XX DR N-PSDB; AA245730.

XX XX

PT New nucleic acid molecule encoding an enzyme involved in lignan  
 XX biosynthetic pathway, useful for producing large amounts of lignans  
 PF Claim 8; Page 46-47; 66pp; English.  
 PR  
 XX  
 CC The present sequence represents a secoisolariciresinol dehydrogenase  
 CC protein. The enzyme is involved in the lignan biosynthetic pathway.  
 CC The secoisolariciresinol dehydrogenase proteins have a molecular  
 CC weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require  
 CC NAD or NADP as a cofactor. The secoisolariciresinol dehydrogenase  
 CC nucleic acids are used for the recombinant expression of the enzymes.  
 CC It is also used to obtain expression or enhanced expression of  
 CC secoisolariciresinol dehydrogenase in plants or to alter lignan  
 CC biosynthesis. The enzyme is used for production of the pharmacologically  
 CC active lignan, matairesinol. The secoisolariciresinol dehydrogenase  
 CC proteins and nucleic acids can be utilized to: elevate or otherwise  
 CC alter the levels of health-protecting lignans, including phytoestrogens  
 CC such as enterolactone and enterodiol, in plant species, including  
 CC vegetables, grains and fruits and to food items incorporating material  
 CC derived from such genetically altered plants; genetically alter plant  
 CC species to provide an abundant, natural supply of lignans useful for  
 CC a variety of purposes, for example as nutraceuticals and dietary  
 CC supplements; to genetically alter living organisms to produce an  
 CC abundant supply of optically pure lignans having desirable biological  
 CC properties, for example (-)-trachelogenin which possesses antiviral  
 CC properties, and (-)-podophyllotoxin.  
 XX  
 SQ Sequence 273 AA;

Query Match 100.0%; Score 1393; DB 21; Length 273;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-130;  
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQLRTAFARRLEGKVALITGGASIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTS 60  
 DB 1 MQLRTAFARRLEGKVALITGGASIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTS 60

QY 61 NSTYIHCDVTNEDGVKNADVNTVSTYKGLDIFMSNAGISDPNRPRIIDNEKADFERVLSV 120  
 DB 61 NSTYIHCDVTNEDGVKNADVNTVSTYKGLDIFMSNAGISDPNRPRIIDNEKADFERVLSV 120

QY 121 NVTVGFLCMKHAARVMI PARSGNIISTASLSSTMGSSSHAYCGSKHAVLALTRNLAVEL 180  
 DB 121 NVTVGFLCMKHAARVMI PARSGNIISTASLSSTMGSSSHAYCGSKHAVLALTRNLAVEL 180

QY 181 GQFGIRVNCNLSPPGLPTALGKFKSGIKNEEEFENVINFGNKGPKFNVEDVANAALYLA 240  
 DB 181 GQFGIRVNCNLSPPGLPTALGKFKSGIKNEEEFENVINFGNKGPKFNVEDVANAALYLA 240

QY 241 SDEAKYVSGHNLFIDGGFSVCNSVIKVFQYDPS 273  
 DB 241 SDEAKYVSGHNLFIDGGFSVCNSVIKVFQYDPS 273

RESULT 2  
 AAY54420  
 ID AAY54420 standard; Protein; 272 AA.  
 XX AC AAY54420;  
 XX DT 06-APR-2000 (first entry)  
 XX DE Secoisolariciresinol dehydrogenase protein clone DEHY130.  
 KW Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway;  
 KW lignan; matairesinol; health-protecting lignan; phytoestrogen;  
 KW enterolactone; enterodiol; nutraceutical; dietary supplement;  
 KW (-)-trachelogenin; antiviral; (-)-podophyllotoxin.  
 XX OS Forsythia intermedia.  
 XX FN W09955846-A1.  
 XX

PD 04-NOV-1999.  
 XX  
 PF 23-APR-1999; 99WO-US089375.  
 XX  
 PR 24-APR-1998; 98US-0082977.  
 XX  
 PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
 XX  
 PI Xia Z, Costa MA, Davin LB, Lewis NG;  
 XX WPI; 2000-126356/11.  
 DR N-ESDS; AAZ45743.  
 XX  
 PT New nucleic acid molecule encoding an enzyme involved in lignan  
 XX biosynthetic pathway, useful for producing large amounts of lignans  
 XX Example 2; Page 61-63; 66pp; English.  
 CC The present sequence represents a secoisolariciresinol dehydrogenase  
 CC protein. The enzyme is involved in the lignan biosynthetic pathway.  
 CC The secoisolariciresinol dehydrogenase proteins have a molecular  
 CC weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require  
 CC NAD or NADP as a cofactor. The secoisolariciresinol dehydrogenase  
 CC nucleic acids are used for the recombinant expression of the enzymes.  
 CC It is also used to obtain expression or enhanced expression of  
 CC secoisolariciresinol dehydrogenase in plants or to alter lignan  
 CC biosynthesis. The enzyme is used for production of the pharmacologically  
 CC active lignan, matairesinol. The secoisolariciresinol dehydrogenase  
 CC proteins and nucleic acids can be utilized to: elevate or otherwise  
 CC alter the levels of health-protecting lignans, including phytoestrogens  
 CC such as enterolactone and enterodiol, in plant species, including  
 CC vegetables, grains and fruits and to food items incorporating material  
 CC derived from such genetically altered plants; genetically alter plant  
 CC species to provide an abundant, natural supply of lignans useful for  
 CC a variety of purposes, for example as nutraceuticals and dietary  
 CC supplements; to genetically alter living organisms to produce an  
 CC abundant supply of optically pure lignans having desirable biological  
 CC properties, for example (-)-trachelogenin which possesses antiviral  
 CC properties, and (-)-podophyllotoxin.  
 XX  
 SQ Sequence 272 AA;

Query Match 99.6%; Score 1388; DB 21; Length 272;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-130;  
 Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QLRTAFARRLEGKVALITGGASIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSN 61  
 DB 1 QLRTAFARRLEGKVALITGGASIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSN 60

QY 62 STYIHCDVTNEDGVKNADVNTVSTYKGLDIFMSNAGISDPNRPRIIDNEKADFERVLSV 121  
 DB 61 STYIHCDVTNEDGVKNADVNTVSTYKGLDIFMSNAGISDPNRPRIIDNEKADFERVLSV 120

QY 122 VTGVFLCMKHAARVMI PARSGNIISTASLSSTMGSSSHAYCGSKHAVLALTRNLAVEL 181  
 DB 121 VTGVFLCMKHAARVMI PARSGNIISTASLSSTMGSSSHAYCGSKHAVLALTRNLAVEL 180

QY 182 QFGIRVNCNLSPPGLPTALGKFKSGIKNEEEFENVINFGNKGPKFNVEDVANAALYLA 241  
 DB 181 QFGIRVNCNLSPPGLPTALGKFKSGIKNEEEFENVINFGNKGPKFNVEDVANAALYLA 240

QY 242 DEAKYVSGHNLFIDGGFSVCNSVIKVFQYDPS 273  
 DB 241 DEAKYVSGHNLFIDGGFSVCNSVIKVFQYDPS 272

RESULT 3  
 AAY54413  
 ID AAY54413 standard; Protein; 277 AA.  
 XX AC AAY54413;  
 XX

|          |                                                                          |               |  |
|----------|--------------------------------------------------------------------------|---------------|--|
| DT       | 06-APR-2000                                                              | (first entry) |  |
| DE       | Secoisolariciresinol dehydrogenase protein clone SMDEHY321.              |               |  |
| XX       | Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway;         |               |  |
| KW       | lignan; matairesinol; health-protecting lignan; phytoestrogen;           |               |  |
| KW       | enterolactone; enterodiol; neutriceutical; dietary supplement;           |               |  |
| KW       | (-)-trachelogenin; antiviral; (-)-podophyllotoxin.                       |               |  |
| XX       | Forsythia intermedia.                                                    |               |  |
| XX       | WO9955846-A1.                                                            |               |  |
| XX       | 04-NOV-1999.                                                             |               |  |
| XX       | 23-APR-1999;                                                             | 99WO-US08975. |  |
| XX       | 24-APR-1998;                                                             | 98US-0082977. |  |
| XX       | (UNIW ) UNIV WASHINGTON STATE RES FOUND.                                 |               |  |
| XX       | Xia Z, Costa MA, Davin LB, Lewis NG;                                     |               |  |
| XX       | WPI; 2000-126356/11.                                                     |               |  |
| DR       | N-PSDB; AAZ45731.                                                        |               |  |
| XX       | New nucleic acid molecule encoding an enzyme involved in lignan          |               |  |
| PT       | biosynthetic pathway, useful for producing large amounts of lignans      |               |  |
| PT       | Claim 8; Page 49-50; 66pp; English.                                      |               |  |
| PS       | The present sequence represents a secoisolariciresinol dehydrogenase     |               |  |
| XX       | protein. The enzyme is involved in the lignan biosynthetic pathway.      |               |  |
| CC       | The secoisolariciresinol dehydrogenase proteins have a molecular         |               |  |
| CC       | weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require       |               |  |
| CC       | NAD or NADP as a cofactor. The secoisolariciresinol dehydrogenase        |               |  |
| CC       | nucleic acids are used for the recombinant expression of the enzymes.    |               |  |
| CC       | It is also used to obtain expression or enhanced expression of           |               |  |
| CC       | secoisolariciresinol dehydrogenase in plants or to alter lignan          |               |  |
| CC       | biosynthesis. The enzyme is used for production of the pharmacologically |               |  |
| CC       | active lignan, matairesinol. The secoisolariciresinol dehydrogenase      |               |  |
| CC       | proteins and nucleic acids can be utilized to: elevate or otherwise      |               |  |
| CC       | alter the levels of health-protecting lignans, including phytoestrogens  |               |  |
| CC       | such as enterolactone and enterodiol, in plant species, including        |               |  |
| CC       | vegetables, grains and fruits and to food items incorporating material   |               |  |
| CC       | derived from such genetically altered plants; genetically alter plant    |               |  |
| CC       | species to provide an abundant, natural supply of lignans useful for     |               |  |
| CC       | a variety of purposes, for example as neutriceuticals and dietary        |               |  |
| CC       | supplements; to genetically alter living organisms to produce an         |               |  |
| CC       | abundant supply of optically pure lignans having desirable biological    |               |  |
| CC       | properties, for example (-)-trachelogenin which possesses antiviral      |               |  |
| CC       | properties, and (-)-podophyllotoxin.                                     |               |  |
| XX       |                                                                          |               |  |
| SQ       | Sequence 277 AA;                                                         |               |  |
|          | Query Match 97.9%; Score 1364; DB 21; Length 277;                        |               |  |
|          | Best Local Similarity 98.2%; Pred. No. 1.8e-127;                         |               |  |
|          | Matches 267; Conservative 1; Mismatches 4; Indels 0; Gaps 0;             |               |  |
| Qy       | 2 QLRFAARRLEKGVALLTGASGIGETTAKLFSQHGAKVAIADVQDELGHWSVEAIGTSN 61          |               |  |
| Db       | 6 QVLTAAARRLEKGVALLTGASGIGETTAKLFSQHGAKVAIADVQDELGHWSVEAIGTSN 65         |               |  |
| Qy       | 62 STYIHCVDVTNEDGVKNVAVNTVSTYTGKLDIFNSNAGISDPNRIIDNEKADFERSVSN 121       |               |  |
| Db       | 66 STYIHCVDVTNEDGVKNVAVNTVSTYTGKLDIFNSNAGISDPNRIIDNEKADFERSVSN 125       |               |  |
| Qy       | 122 VTGFLCMKHAAKVMIPARSGNIISTASLSMTGSGSHAYCGSKHVALTRNLAVELG 181          |               |  |
| Db       | 126 VTGFLCMKHAAKVMIPARSGNIISTASLSMTGSGSHAYCGSKHVALTRNLAVELG 185          |               |  |
| Qy       | 182 QFGRVNCNLSPPGLPTALGKFKSGIKNEEFENVINPAGNLKGPKNVEDVANALYLAS 241        |               |  |
| Db       | 186 QFGRVNCNLSPPGLPTALGKFKSGIKNEEFENVINPAGNLKGPKNVEDVANALYLAS 245        |               |  |
| Qy       | 242 DEAKYVSGHNLFDIDGGFSVCNSVIKVFQYFDS 273                                |               |  |
| Db       | 246 DEAKYVSGHNLFDIDGGFSVCNSVIKVFQYFDS 277                                |               |  |
| RESULT 4 |                                                                          |               |  |
| AY54416  |                                                                          |               |  |
| ID       | AAV54416 standard; Protein; 276 AA.                                      |               |  |
| XX       | AAV54416;                                                                |               |  |
| AC       | 06-APR-2000 (first entry)                                                |               |  |
| XX       | Secoisolariciresinol dehydrogenase protein clone SMDEHY631.              |               |  |
| XX       | Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway;         |               |  |
| KW       | lignan; matairesinol; health-protecting lignan; phytoestrogen;           |               |  |
| KW       | enterolactone; enterodiol; neutriceutical; dietary supplement;           |               |  |
| KW       | (-)-trachelogenin; antiviral; (-)-podophyllotoxin.                       |               |  |
| XX       | Forsythia intermedia.                                                    |               |  |
| OS       | WO9955846-A1.                                                            |               |  |
| XX       | 04-NOV-1999.                                                             |               |  |
| XX       | 23-APR-1999;                                                             | 99WO-US08975. |  |
| XX       | 24-APR-1998;                                                             | 98US-0082977. |  |
| XX       | (UNIW ) UNIV WASHINGTON STATE RES FOUND.                                 |               |  |
| XX       | Xia Z, Costa MA, Davin LB, Lewis NG;                                     |               |  |
| XX       | WPI; 2000-126356/11.                                                     |               |  |
| DR       | N-PSDB; AAZ45734.                                                        |               |  |
| XX       | New nucleic acid molecule encoding an enzyme involved in lignan          |               |  |
| PT       | biosynthetic pathway, useful for producing large amounts of lignans      |               |  |
| PT       | Claim 8; Page 56-57; 66pp; English.                                      |               |  |
| PS       | The present sequence represents a secoisolariciresinol dehydrogenase     |               |  |
| XX       | protein. The enzyme is involved in the lignan biosynthetic pathway.      |               |  |
| CC       | The secoisolariciresinol dehydrogenase proteins have a molecular         |               |  |
| CC       | weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require       |               |  |
| CC       | NAD or NADP as a cofactor. The secoisolariciresinol dehydrogenase        |               |  |
| CC       | nucleic acids are used for the recombinant expression of the enzymes.    |               |  |
| CC       | It is also used to obtain expression or enhanced expression of           |               |  |
| CC       | secoisolariciresinol dehydrogenase in plants or to alter lignan          |               |  |
| CC       | biosynthesis. The enzyme is used for production of the pharmacologically |               |  |
| CC       | active lignan, matairesinol. The secoisolariciresinol dehydrogenase      |               |  |
| CC       | proteins and nucleic acids can be utilized to: elevate or otherwise      |               |  |
| CC       | alter the levels of health-protecting lignans, including phytoestrogens  |               |  |
| CC       | such as enterolactone and enterodiol, in plant species, including        |               |  |
| CC       | vegetables, grains and fruits and to food items incorporating material   |               |  |
| CC       | derived from such genetically altered plants; genetically alter plant    |               |  |
| CC       | species to provide an abundant, natural supply of lignans useful for     |               |  |
| CC       | a variety of purposes, for example as neutriceuticals and dietary        |               |  |
| CC       | supplements; to genetically alter living organisms to produce an         |               |  |
| CC       | abundant supply of optically pure lignans having desirable biological    |               |  |
| CC       | properties, for example (-)-trachelogenin which possesses antiviral      |               |  |
| CC       | properties, and (-)-podophyllotoxin.                                     |               |  |
| XX       |                                                                          |               |  |
| SQ       | Sequence 276 AA;                                                         |               |  |
|          | Query Match 88.5%; Score 1233; DB 21; Length 276;                        |               |  |
|          | Best Local Similarity 88.2%; Pred. No. 2.1e-114;                         |               |  |
|          | Matches 240; Conservative 14; Mismatches 18; Indels 0; Gaps 0;           |               |  |
| Qy       | 2 QLRFAARRLEKGVALLTGASGIGETTAKLFSQHGAKVAIADVQDELGHWSVEAIGTSN 61          |               |  |

Db 5 QLTAFARLEGGKVALITGGASGGEVTAQLPSQHGAKVAIADVODELGHVSVEAIGLSN 64  
 QY 62 STYIHCDVTNEDGVKNAVDNTVSTYTKGLDIMFNSNAGISDPNRPRIIDNEKADFERVLSVN 121  
 Db 65 STYIHCDVTNEDGVKNAVDNTVSTYTKGLDIMFNNAGISDPYKPRVIDNEKADFERVLSVN 124  
 QY 122 VTGVFLCMKHAARVMIPARSGNIIISTASLSSTMGSGSHAYCGSKHVAVLALTRNLAVELG 181  
 Db 125 VTGVFLCMKHAARVMIPARSGCIIISTASLSSTMGSGSHAYCGSKHVAVLGLTRNLAVELG 184  
 QY 182 QFGIRVNCCLSPFGLPTALCKFKSGIKNEEPEENVINFAGNLKGPKFNVEDVANAALYLAS 241  
 Db 185 QFGIRVNCCLSPFGLPTPLAKKFTGIENDEDLANGIERAGNLKGTKLRIEDVANAALFLAS 244  
 QY 242 DEAKYVSGHNLFTIDGGFVSCNSVIKVOYQPD 273  
 Db 245 DEAQYVSGQNLFTIDGGFVSCNSAIKLFQYDPS 276  
 RESULT 5  
 AAO21494  
 ID AAO21494 standard; Protein; 276 AA.  
 AC AAO21494;  
 XX  
 DT 15-AUG-2002 (first entry)  
 DE  
 DE Secoisolariciresinol dehydrogenase protein.  
 DE  
 KW Guaiacyl (G)-lignan; monocotyledon plant; rice; food additive;  
 KW seed-specific transcriptional regulatory region; dehydrogenase; enzyme.  
 XX Unidentified.  
 OS  
 XX WO200220548-A1.  
 PN  
 XX 14-MAR-2002.  
 PD  
 XX 04-SEP-2001; 2001WO-US27500.  
 PF  
 XX 07-SEP-2000; 2000US-230632P.  
 PR  
 XX (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
 PA (PHYT-) APPLIED PHYTOLOGICS INC.  
 XX  
 PI Lewis NG, Davin LB, Huang N;  
 XX  
 XX WPI; 2002-425767/45.  
 DR N-PSDB; AAL38432.  
 XX  
 XX Increasing guaiacyl-lignan content in monocotyledon plants, by  
 FT transforming plant with chimeric gene construct having seed-specific  
 FT transcriptional regulator linked to gene encoding protein involved in  
 FT G-lignan formation  
 XX  
 XX Claim 2; Fig 10; 136pp; English.  
 PS  
 XX The invention relates to a method for increasing the guaiacyl (G)-lignan  
 CC content in seeds of a monocotyledon plant, comprising selecting at least  
 CC one protein or enzyme integral to the pathway leading to G-lignan  
 CC formation, stably transforming a monocotyledon plant with chimeric gene  
 CC (CG) constructs having a seed-specific transcriptional regulatory region  
 CC operably linked to a nucleic acid sequence encoding the enzyme. The  
 CC method of the invention is useful for stably transforming a  
 CC monocotyledonous plant (e.g. rice) with CG constructs resulting in  
 CC increased expression of the genes encoded by CG constructs. The G-lignan  
 CC enriched seed composition is useful as a food additive. This  
 CC sequence represents the secoisolariciresinol dehydrogenase protein  
 CC relating to the invention.  
 XX  
 XX Sequence 276 AA;  
 SQ

Query Match 88.5%; Score 1233; DB 23; Length 276;  
 Best Local Similarity 88.2%; Pred. No. 2.1e-114; Indels 0; Gaps 0;  
 Matches 240; Conservative 14; Mismatches 18;  
 QY 2 QLTAFARLEGGKVALITGGASGIGETTAKLPQSHGAKVAIADVODELGHVSVEAIGTSN 61  
 Db 5 QLTAFARLEGGKVALITGGASGGEVTAQLPSQHGAKVAIADVODELGHVSVEAIGLSN 64  
 QY 62 STYIHCDVTNEDGVKNAVDNTVSTYTKGLDIMFNSNAGISDPNRPRIIDNEKADFERVLSVN 121  
 Db 65 STYIHCDVTNEDGVKNAVDNTVSTYTKGLDIMFNNAGISDPYKPRVIDNEKADFERVLSVN 124  
 QY 122 VTGVFLCMKHAARVMIPARSGNIIISTASLSSTMGSGSHAYCGSKHVAVLALTRNLAVELG 181  
 Db 125 VTGVFLCMKHAARVMIPARSGCIIISTASLSSTMGSGSHAYCGSKHVAVLGLTRNLAVELG 184  
 QY 182 QFGIRVNCCLSPFGLPTALCKFKSGIKNEEPEENVINFAGNLKGPKFNVEDVANAALYLAS 241  
 Db 185 QFGIRVNCCLSPFGLPTPLAKKFTGIENDEDLANGIERAGNLKGTKLRIEDVANAALFLAS 244  
 QY 242 DEAKYVSGHNLFTIDGGFVSCNSVIKVOYQPD 273  
 Db 245 DEAQYVSGQNLFTIDGGFVSCNSAIKLFQYDPS 276  
 RESULT 6  
 AAY54414  
 ID AAY54414 standard; Protein; 273 AA.  
 AC AAY54414;  
 XX  
 DT 06-APR-2000 (first entry)  
 DE  
 DE Secoisolariciresinol dehydrogenase protein clone SMDEHY431.  
 XX  
 KW Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway;  
 KW lignan; metairesinol; health-protecting lignan; phytoestrogen;  
 KW enterolactone; enterodiol; neutriceutical; dietary supplement;  
 KW (-)-trachelogenin; antiviral; (-)-podophyllotoxin.  
 XX  
 OS Forsythia intermedia.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 120  
 FT Misc-difference 122 /note= "encoded by GTN"  
 FT Misc-difference 122 /note= "encoded by GTN"  
 FT  
 XX WO9955846-A1.  
 PN  
 XX 04-NOV-1999.  
 XX  
 XX 23-APR-1999; 99WO-US08975.  
 XX  
 XX 24-APR-1998; 98US-0082977.  
 XX  
 XX (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
 PA  
 XX Xia Z, Costa MA, Davin LB, Lewis NG;  
 PI  
 XX WPI; 2000-126356/11.  
 DR N-PSDB; AAZ45732.  
 XX  
 XX New nucleic acid molecule encoding an enzyme involved in lignan  
 PT biosynthetic pathway, useful for producing large amounts of lignans  
 XX  
 XX Claim 8; Page 51-52; 66pp; English.  
 PS  
 XX The present sequence represents a secoisolariciresinol dehydrogenase  
 CC protein. The enzyme is involved in the lignan biosynthetic pathway.  
 CC The secoisolariciresinol dehydrogenase proteins have a molecular  
 CC weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require  
 CC NAD or NADP as a cofactor. The secoisolariciresinol dehydrogenase

CC nucleic acids are used for the recombinant expression of the enzymes.  
 CC It is also used to obtain expression or enhanced expression of  
 CC secoisolariciresinol dehydrogenase in plants or to alter lignan  
 CC biosynthesis. The enzyme is used for production of the pharmacologically  
 CC active lignan, matairesinol. The secoisolariciresinol dehydrogenase  
 CC proteins and nucleic acids can be utilized to: elevate or otherwise  
 CC alter the levels of health-protecting lignans, including phytoestrogens  
 CC such as enterolactone and enterodiol, in plant species, including  
 CC vegetables, grains and fruits and to food items incorporating material  
 CC derived from such genetically altered plants; genetically alter plant  
 CC species to provide an abundant, natural supply of lignans useful for  
 CC a variety of purposes, for example as nutraceuticals and dietary  
 CC supplements; to genetically alter living organisms to produce an  
 CC abundant supply of optically pure lignans having desirable biological  
 CC properties, for example (-)-trachelogenin which possesses antiviral  
 CC properties, and (-)-podophyllotoxin.  
 XX  
 SQ Sequence 273 AA;  
 Query Match 87.8%; Score 1223; DB 21; Length 273;  
 Best Local Similarity 86.8%; Pred. No. 2e-113;  
 Matches 237; Conservative 15; Mismatches 21; Indels 0; Gaps 0;  
 Qy 1 MQLRTAFARRLEGKVALITGGASGIGETAKLFSQHGAKVAIADVQDELGHSVVEAIGTS 60  
 Db 1 MQLRTAARRLEGKVALITGGASGIGETAKLFSQHGAKVAIADVQDELGHSVVEAIGPS 60  
 Qy 61 NSTYHCDVTNEDGVKNADVNTVSTYKGLDIFMSNAGISDPNRPRIIDNEKADFERVLSV 120  
 Db 61 NSTYHCDVTNEDGVKNADVNTVSTYKGLDIFMSNAGISDPYKPRIVDNEKADFERVLSX 120  
 Qy 121 NVTGFLCMKHAARVMIPARSGNIISTASLSTWGGSSHAYCGSKHVALALTRNLAVEL 180  
 Db 121 NXTGVFLPMKHAARIMVPARNGCIISTASLSTWGGSSHAYCGKHAVALGLTRNLAVEL 180  
 Qy 181 QGFGIRVNCCLSPFGLPTALGKFKSGIKNEEBEFENVINPAGNLKGFKNVEDVANAALYLA 240  
 Db 181 QGFGIRVNCCLSPFGLPTALGKFKSGIENDVDFAAIEHAGNLKGTKLRIEDVANAALFLA 240  
 Qy 241 SDEAKYVSGHNLFDIDGFSVCNSVTKVFPYDPS 273  
 Db 241 SDEAKYVSGQNLFDIDGFSVCNSAIKMFQYDPS 273  
 RESULT 7  
 AAY54415  
 ID AAY54415 standard; Protein; 277 AA.  
 XX  
 AC AAY54415;  
 XX  
 DT 06-APR-2000 (first entry)  
 XX  
 DE Secoisolariciresinol dehydrogenase protein clone SMDEHY511.  
 XX  
 KW Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway;  
 KW lignan; matairesinol; health-protecting lignan; phytoestrogen;  
 KW enterolactone; enterodiol; nutraceutical; dietary supplement;  
 KW (-)-trachelogenin; antiviral; (-)-podophyllotoxin.  
 XX  
 OS Forsythia intermedia.  
 XX  
 FN WO9955846-A1.  
 XX  
 PD 04-NOV-1999.  
 XX  
 PF 23-APR-1999; 99WO-US089975.  
 XX  
 PR 24-APR-1998; 98US-0082977.  
 XX  
 PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
 XX  
 FI Xia Z, Costa MA, Davin LB, Lewis NG;  
 XX

DR WPI; 2000-126356/11.  
 XX N-PSDB; AAZ45733.  
 PT New nucleic acid molecule encoding an enzyme involved in lignan  
 XX biosynthetic pathway, useful for producing large amounts of lignans -  
 PS Claim 8; Page 54-55; 66pp; English.  
 XX  
 CC The present sequence represents a secoisolariciresinol dehydrogenase  
 CC protein. The enzyme is involved in the lignan biosynthetic pathway.  
 CC The secoisolariciresinol dehydrogenase proteins have a molecular  
 CC weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require  
 CC NAD or NADP as a cofactor. The secoisolariciresinol dehydrogenase  
 CC nucleic acids are used for the recombinant expression of the enzymes.  
 CC It is also used to obtain expression or enhanced expression of  
 CC secoisolariciresinol dehydrogenase in plants or to alter lignan  
 CC biosynthesis. The enzyme is used for production of the pharmacologically  
 CC active lignan, matairesinol. The secoisolariciresinol dehydrogenase  
 CC proteins and nucleic acids can be utilized to: elevate or otherwise  
 CC alter the levels of health-protecting lignans, including phytoestrogens  
 CC such as enterolactone and enterodiol, in plant species, including  
 CC vegetables, grains and fruits and to food items incorporating material  
 CC derived from such genetically altered plants; genetically alter plant  
 CC species to provide an abundant, natural supply of lignans useful for  
 CC a variety of purposes, for example as nutraceuticals and dietary  
 CC supplements; to genetically alter living organisms to produce an  
 CC abundant supply of optically pure lignans having desirable biological  
 CC properties, for example (-)-trachelogenin which possesses antiviral  
 CC properties, and (-)-podophyllotoxin.  
 XX  
 SQ Sequence 277 AA;  
 Query Match 84.4%; Score 1175; DB 21; Length 277;  
 Best Local Similarity 83.5%; Pred. No. 1.3e-108;  
 Matches 227; Conservative 20; Mismatches 25; Indels 0; Gaps 0;  
 Qy 2 QLRTAFARRLEGKVALITGGASGIGETAKLFSQHGAKVAIADVQDELGHSVVEAIGTSN 61  
 Db 6 QVLTAITRRLEGKVALITGGASGIGETAKLFSQHGAKVAIADVQDELGHSVVEAIGTSN 65  
 Qy 62 STYHCDVTNEDGVKNADVNTVSTYKGLDIFMSNAGISDPNRPRIIDNEKADFERVLSVN 121  
 Db 66 SIYHCDVTNEDDVKNAVDNTVSTYKGLDIFMNFAGIADPNKPRIVDNEKADFERVLSVN 125  
 Qy 122 VTGVFLCMKHAARVMIPARSGNIISTASLSTWGGSSHAYCGSKHVALALTRNLAVELG 181  
 Db 126 VTGVFLCMKHAARVMVPARSGSIISTASVSTIGGAASHAYCCSKHVALGLTRNLAVELG 185  
 Qy 182 QFGIRVNCCLSPFGLPTALGKFKSGIKNEEBEFENVINPAGNLKGFKNVEDVANAALYLA 241  
 Db 186 QFGIRVNCCLAPYALATPLAKKFVGLNEDDELENAMSLMGNLKGTLNKAEDVANAALYLA 245  
 Qy 242 DEAKYVSGHNLFDIDGFSVCNSVTKVFPYDPS 273  
 Db 246 DEAKYVSGHNLFDIDGFSVYNSAIKMFQYDPT 277  
 RESULT 8  
 ABB91329  
 ID ABB91329 standard; Protein; 285 AA.  
 XX  
 AC ABB91329;  
 XX  
 DT 31-MAY-2002 (first entry)  
 XX  
 DE Herbicidally active polypeptide SEQ ID NO 540.  
 XX  
 KW Herbicidal; plant; agriculture; herbicide.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 FN WO200210210-A2.  
 XX

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PD 07-FEB-2002.
XX
XX 28-AUG-2001; 2001WO-EP09892.
XX
XX 28-AUG-2001; 2001WO-EP09892.
XX
XX (FARB ) BAYER AG.
XX
XX Tietjen K, Weidler M;
XX
XX WPI; 2002-269010/31.
XX
XX Identifying plant target proteins for herbicidally active compounds,
XX comprising aligning and comparing nucleic acid or amino acid sequences
XX from plant with nucleic acid or amino acid sequences from non-plant
XX organisms -
XX
XX Claim 5; SEQ ID NO 540; 261pp + Sequence Listing; English.
XX
XX The invention relates to identifying target proteins
XX (ABB90790-ABB94016) for herbicidally active compounds, comprising
XX aligning and comparing nucleic acid or amino acid sequences from plant
XX with nucleic acid or amino acid sequences from non-plant organisms using
XX suitable search parameters, where plant sequences having an E-value
XX greater by a factor of 3 than the E-value of most similar non-plant
XX sequences are selected. The polypeptides or nucleic acids encoding them
XX are useful for identifying modulators. The identified modulators are
XX useful as herbicides.
XX
XX SQ Sequence 285 AA;
XX
XX Query Match 47.3%; Score 658.5; DB 23; Length 285;
XX Best Local Similarity 50.9%; Pred. No. 4.4e-57;
XX Matches 139; Conservative 43; Mismatches 78; Indels 13; Gaps 5;
XX
XX QY 8 ARRLGKVALITGASGIGETAKFQHQKAKVAIADVDLGHVSVEAI--GTSNST-- 63
XX Db :
XX 15 SORLLGKVALITGATGIGESIVRLFHKHAKVCIVDLQDLGGVCKSLRGSKETAF 74
XX
XX QY 64 YIHCDVTNEDGVKNVNDVTSTYTKLIDIMFSNAGISDENPRIIDNEKADPERVLSNVVT 123
XX Db :
XX 75 FIHGDVREDDISNAVDFAVKNGFTLIDLNAGLCGAPCPDIRNYSLSSEPFMTFDVNVK 134
XX
XX QY 124 GVFLCKHAAHVMIIPARSGNIISTASLSTMGSSGHAYCGSKHAVLALTNLAVELGQF 183
XX Db :
XX 135 GAFLSMKHAAHVMIPEKKSIVSLCSGVGVGVGPHSVGSKHAVLGLTFSVAELGQH 194
XX
XX QY 184 GIRVNCISPLGLTALCKPFGSKNKEEPEENVI---NFA---GNLKPKNVEDVANAA 236
XX Db :
XX 195 GIRVNCVSPFAVAKLA--LAHLPEERTEDEAFVGRFNAANLNKGVLTVDVANAV 252
XX
XX QY 237 LYLASDEAKVSGHNLFDIGGFSVCNSVIKVFQ 269
XX Db :
XX 253 LFLASDDSRVYISGDLNLMIDGGFTCTNHSFKVPR 285
XX
XX RESULT 9
XX ID AAG25524 standard; Protein; 285 AA.
XX AC
XX AAAG25524;
XX
XX DT 17-OCT-2000 (first entry)
XX
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 29625.
XX
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX
XX OS Arabidopsis thaliana.
XX
XX 'PN EP1033405-A2.

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XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121925.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127462.
XX 06-APR-1999; 99US-0128234.
XX 08-APR-1999; 99US-0128714.
XX 16-APR-1999; 99US-0129845.
XX 19-APR-1999; 99US-0130077.
XX 21-APR-1999; 99US-0130449.
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| Db                                                              | 15           | SQRLGKVALITGGATGIGESIVLPHKHKAKVCIVDQDDLGGEVCKSLRGESKETAF 74      |
| Qy                                                              | 64           | YIHCDVTNEDGVKNAVDNTVSTYGLDIMFSNAGISDPNRPRIIDNEKADPERVLSVNV 123   |
| Db                                                              | 75           | PIHGDVREDDISNAVDFAVKNFOTLDLILNAGLCGAPCPDIRNYSILSEFEMTFDNNV 134   |
| Qy                                                              | 124          | GVFLCMKHAARVMIIPARSGNIISTASLSTWGGSSHAYCGSKHAVIALTRNLAVELGQ 183   |
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| Qy                                                              | 184          | GIRVNCLSPECLPTALCKKFSGINKNEEFENVI----NFA---GNLKGPKNFVEDVANAA 236 |
| Db                                                              | 195          | GIRVNCVSPVAVATKLA--LAHLPEERTEDAFVGFRNFAAANANLKGVELTVGDVANAV 252  |
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DE Herbicidally active polypeptide SEQ ID NO 1835.  
 XX Herbicidally active polypeptide SEQ ID NO 1835.  
 KW Herbicidally active polypeptide SEQ ID NO 1835.  
 XX Herbicidally active polypeptide SEQ ID NO 1835.  
 OS Arabidopsis thaliana.  
 XX Arabidopsis thaliana.  
 FN WO200210210-A2.  
 XX WO200210210-A2.  
 PD 07-FEB-2002.  
 XX 07-FEB-2002.  
 XX 28-AUG-2001; 2001WO-EP09892.  
 XX 28-AUG-2001; 2001WO-EP09892.  
 XX (FARB ) BAYER AG.  
 XX Tietjen K, Weidler M;  
 XX WPI; 2002-269010/31.  
 XX Identifying plant target proteins for herbicidally active compounds,  
 PT comprising aligning and comparing nucleic acid or amino acid sequences  
 PT from plant with nucleic acid or amino acid sequences from non-plant  
 PT organisms -  
 XX Claim 5; SEQ ID NO 1835; 261pp + Sequence Listing; English.  
 XX The invention relates to identifying target proteins  
 CC (ABB90790-ABB94016) for herbicidally active compounds, comprising  
 CC aligning and comparing nucleic acid or amino acid sequences from plant  
 CC with nucleic acid or amino acid sequences from non-plant organisms using  
 CC suitable search parameters, where plant sequences having an E-value  
 CC greater by a factor of 3 than the E-value of most similar non-plant  
 CC sequences are selected. The polypeptides or nucleic acids encoding them  
 CC are useful for identifying modulators. The identified modulators are  
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 XX 17-OCT-2000 (first entry)  
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 XX Arabidopsis thaliana protein fragment SEQ ID NO: 20101.

XX Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
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 XX Arabidopsis thaliana.  
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 XX 06-SEP-2000.  
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| Matches 126; Conservative 46; Mismatches 86; Indels 11; Gaps 4; |              |                                                                    |
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| Db                                                              | 32           | SRKLEGKVALITGASIGKATAGKFIHSHGAKVIAIADQIQIGRETQELGPS-CAYPPC 90      |
| Qy                                                              | 68           | DVTNEDCVKNAVNTVSTYCKLDIMFSNAGISDPNRPRIIDNEKADPERVLSVNTGVFL 127     |
| Db                                                              | 91           | DVTKESDIANAVDFAVSLHTKLDIMYNNAGIPCKTPPSIVDLNLFVKINTNVGMA 150        |
| Qy                                                              | 128          | CMKHAARVMIIPARSGNIISTASLSWTMGSGSHAYCGSKHAVLALTRNLAVELQCFQIRV 187   |
| Db                                                              | 151          | GIKHAARVMIIPRNSGSIICAGSVTGMGGLAQHTYSVSKSAVIGIVRSTASELCKHIVR 210    |
| Qy                                                              | 188          | NCLSPFGLPTA-----LGKKFSGIKNEEFENFVINFAGNLKPKFNVEDVANAALYLASD 242    |
| Db                                                              | 211          | NCISPPFAITTSFVWDEMQRQIYPGV-DDSRLIQIVQSTGVNLGVEVCEPTDVANAAYLASD 269 |
| Qy                                                              | 243          | EAKYVSGHNLFDIDGFSVCNSVIKVFQYP 271                                  |
| Db                                                              | 270          | DSKYVNGHNLVVDGGF----TTVKTLDFP 294                                  |

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DT 17-OCT-2000 (first entry)  
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 20100.  
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KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
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Qy 68 DVTNEDGVKNADVNTVSTYKLDIMFNSAGISDPNRPRIIDNEKADPERVLSVNVTVGVL 127
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RESULT 13
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DT 17-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
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PN EP1033405-A2.
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PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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Best Local Similarity 47.0%; Pred No. 5.3e-51;

Matches 126; Conservative 45; Mismatches 86; Indels 11; Gaps 4;

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Db 16 RLLEGKVALITGASGIGETTAKLPFSQHGAKVATADYODELGHVSVEAIGTSNHYHCD 74





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Searched: 328717 seqs, 42310858 residues

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## Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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| 1          | 588.5 | 42.2    | 337 | 1      | US-08-440-856A-3     | Sequence 3, Appli |             |
| 2          | 582.5 | 41.8    | 333 | 1      | US-08-440-856A-4     | Sequence 4, Appli |             |
| 3          | 500   | 35.9    | 359 | 1      | US-08-440-856A-8     | Sequence 8, Appli |             |
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| 6          | 369   | 26.5    | 256 | 4      | US-09-504-358-14     | Sequence 14, Appl |             |
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| 42 | 42 | 279   | 20.0 | 203 | 4 | US-09-634-955B-26    | Sequence 26, Appl  |
| 43 | 43 | 279   | 20.0 | 203 | 4 | US-09-634-955B-17    | Sequence 17, Appl  |
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## ALIGNMENTS

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RESULT 2  
 US-08-440-856A-4  
 ; Sequence 4, Application US/08440856A  
 ; Patent No. 5750873  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DELLAPORTA, STEPHEN L.  
 ; TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING  
 ; TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: MORRISON & FOERSTER  
 ; STREET: 2000 PENNSYLVANIA AVE. N.W.  
 ; CITY: WASHINGTON  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20037  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/440,856A  
 ; FILING DATE: 15-MAY-1995  
 ; CLASSIFICATION: 800  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: MILLMAN, ROBERT A.  
 ; REGISTRATION NUMBER: 36,217  
 ; REFERENCE/DOCKET NUMBER: 05463-20001.00  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 887-1517  
 ; TELEFAX: (202) 887-0763  
 ; TELEX: 706141  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 333 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear

US-08-440-856A-4  
 Query Match 41.8%; Score 582.5; DB 1; Length 333;  
 Best Local Similarity 42.2%; Pred. No. 1.4e-54;  
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US-08-440-856A-8  
 ; Sequence 8, Application US/08440856A  
 ; Patent No. 5750873  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DELLAPORTA, STEPHEN L.  
 ; TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING  
 ; TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: MORRISON & FOERSTER  
 ; STREET: 2000 PENNSYLVANIA AVE. N.W.  
 ; CITY: WASHINGTON  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20037  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/440,856A  
 ; FILING DATE: 15-MAY-1995  
 ; CLASSIFICATION: 800  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: MILLMAN, ROBERT A.  
 ; REGISTRATION NUMBER: 36,217  
 ; REFERENCE/DOCKET NUMBER: 05463-20001.00  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 887-1517  
 ; TELEFAX: (202) 887-0763  
 ; TELEX: 706141  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 359 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide

US-08-440-856A-8  
 Query Match 35.9%; Score 500; DB 1; Length 359;  
 Best Local Similarity 38.8%; Pred. No. 1.3e-45;  
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; TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIATES
; FILE REFERENCE: BC1001 US NA
; CURRENT APPLICATION NUMBER: US/09/954,314
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/120,702
; PRIOR FILING DATE: 1999-February-19
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 14
; LENGTH: 256
; TYPE: PR1
; ORGANISM: Brevibacterium sp HCU
; US-09-954-314-14

Query Match 26.5%; Score 369; DB 4; Length 256;
Best Local Similarity 35.7%; Pred. No. 1.2e-31;
Matches 91; Conservative 55; Mismatches 101; Indels 8; Gaps 5;

Qy 10 RLEGKVALITGGASGIGETTAKLFSOHGAKVAIAVDQDELGHVSVEAIGTSN--STYIHC 67
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3 RLGKVAIVITGGAAGMGRIGQSELYASEGAQVAVDVNEQEGRATADAIRASGGVANYWKL 62
Qy 68 DVTNEDGVKNVAVNTVSTYCKLIDMFNSNAGISDPNRPRIIDNEKADPERVLSVNVTVGVFL 127
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
63 DVSDESEVETWSDIAKREGAINVLVNNAGVTGADKPTHEIDER-DLDELVLVDVKGVPF 121
Qy 128 CMKHAARVMPARSNGNIISTASLSSTMGSGSHAYCGSKHVALTRNLAVELGQFGRV 187
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
122 MTKHCIPYKQAGGAIVNFAIYGLVGSQELTPHAAKGAVALTKQDAVTVGPSNIRV 181
Qy 188 NCLSPCLPTALGKKGSGIKNEEPEENVINPAGNLKGPKNV---EDVANAALYLASDEA 244
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
182 NAVAPGTILTPVKEL-GRGPDGLDGYTKLMG-AKGPLGRVTPPEVAAATFLASEEA 239
Qy 245 KYVSGHNLFTDGGFS 259
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
240 SFTIGAVLPVDGGYT 254

RESULT 8
US-09-198-452A-309
; Sequence 309, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 309
; LENGTH: 251
; TYPE: PR1
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-309

Query Match 25.6%; Score 357; DB 4; Length 251;
Best Local Similarity 33.5%; Pred. No. 2.2e-30;
Matches 87; Conservative 53; Mismatches 92; Indels 28; Gaps 6;

Qy 11 LEGKVALITGGASGIGETTAKLFSOHGAKVAIAVDQDELGHVSVEAI-GTSNS-TYIHC 68
Db 8 LVGKVVITGSGRIGLIGVVKLFLENGADVEIWLNEERGOAVIESLTGLGGEVSFARV 67
Qy 69 VTNEDGVKNVAVNTVSTYCKLIDMFNSNAGISDPNRPRIIDNEKADPERVLSVNVTVGVFLC 128
Db 68 VSHNGVCVKQKFLDKHKKIILVNNAGITFDN--LLMRSEDDQSVISTNLSLYYT 125
Qy 129 MKHAARVMPARSNGNIISTASLSSTMGSGSHAYCGSKHVALTRNLAVELGQFGRV 188
Db 126 CSSVIRHMKARSGSLINVASIVAKIGSAGQNTYAAKAGATFKSLAKEAARNIRVN 185
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Qy 189 CLSPFGLPTALGKKGSGIKNEEPEENVINPAGNLK-----GPKFNVEDVANAALYL 239
Db 186 CLAPGFI-----ETDMSVLN--DNLKAELKSIPLGRAGTPEDEVARVALFL 230
Qy 240 ASDEAKYVSGHNLFTDGGFS 259
Db 231 ASQLSSYMTAQTIVVDGGLT 250

RESULT 9
US-09-328-352-7731
; Sequence 7731, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7731
; LENGTH: 261
; TYPE: PR1
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7731

Query Match 25.3%; Score 352; DB 4; Length 261;
Best Local Similarity 34.5%; Pred. No. 8.2e-30;
Matches 89; Conservative 53; Mismatches 104; Indels 12; Gaps 4;

Qy 11 LEGKVALITGGASGIGETTAKLFSOHGAKVAIAVDQDELGHVSVEAIGTS--NSTYIHC 68
Db 5 LDGKVAFITGSASGIGLEIAKKAQAGAKVVISDMNAEKCOETASSLKERGFDAISAPCD 64
Qy 69 VTNEDGVKNVAVNTVSTYCKLIDMFNSNAGISDPNRPRIIDNEKADPERVLSVNVTVGVFLC 128
Db 65 VTDEDAYKQAIETLTKTFTGVDILINNAGFQ--HVAPIEEFPFIAVFKLVQVMLTGAFIG 122
Qy 129 MKHAARVMPARSNGNIISTASLSSTMGSGSHAYCGSKHVALTRNLAVELGQFGRV 188
Db 123 IKHVFPMKAQKYGRINNASINGLIGFAGKAGYNSAKHGVIGLTKVAALECARDGITVN 182
Qy 189 CLSPFGLPTALGK-----KFSGKNEEPEENVINPAGNLKGPKNVEDVANAALYLAS 241
Db 183 ALCPGVVDTPLVRGQIADLAKTRNVSLDSELDVI-LAMVPQKLLSVEEADIYTIPLAS 241
Qy 242 DEAKYVSGHNLFTDGGFS 259
Db 242 SKAGGVITQAVVMDGGYT 259

RESULT 10
US-09-363-189B-6
; Sequence 6, Application US/09363189B
; Patent No. 6242228
; GENERAL INFORMATION:
; APPLICANT: SUGIYAMA, MASAKAZU
; APPLICANT: TONOUCHI, NAOTO
; APPLICANT: SUZUKI, SHUNICHI
; APPLICANT: YOKOZEKI, KENZO
; TITLE OF INVENTION: XYLITOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF
; FILE REFERENCE: 0010-1024-0
; CURRENT APPLICATION NUMBER: US/09/363,189B
; CURRENT FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: JP10-216047
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 262
; TYPE: PR1
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; TYPE: PRT
; ORGANISM: Bacillus subtilis
; US-940-019-29

Query Match      24.5%; Score 341.5; DB 4; Length 261;
Best Local Similarity 34.4%; Pred. No. 1.1e-28;
Matches 93; Conservative 50; Mismatches 98; Indels 29; Gaps 10;

Qy 11 LEGKVALITGGASGIGETTAKLFSOHGAKVAI---ADVQD--ELGHSVVEAIGTSNSTVI 65
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 5 LKGVVAITGAASGLGKAMAIRFGKEQAKVINYNSKQDPNEVKEEVIKAGG--EAVVV 62
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 66 HCDVTNEDGVKNVAVNTVSTYKLDIMFSNAGISDPNRPRIIDNEK--ADPERVLSVNT 123
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 63 QGDTVTEEDVKNIQVTAIKEFGTLDIMINNAGLENP---VPSHEMLPKDWDKVIQTNLT 118
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 124 GVFLCKMKAARVMIPAR-SGNIISTASISSTWGGSSHAYCGSKHVALATRLNLAVELGQ 182
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 119 GAFGLSREAIKYFVENDIKGNVINSSVHEVWPFLFVHYAASKGKIKMTETLALAYAP 178
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 183 FGIRVNCCLSPFLPTAL-CKKESGINKNEEPEENVINPAGNLKGPKNVEDVANAALYLAS 241
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 179 KGRVNNIGPGAINTPINAKEFADPKQADVESMIPM-GYIGEP-----EIAAVALAS 233
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 242 DEAKYVSGHNLFIDGFSVCNSVIKFOYP 271
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 234 KEASYVTGITLFDGGM-----QYP 254
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
US-09-940-037A-29
; Sequence 29, Application US/09940037A
; Patent No. 6485948
; GENERAL INFORMATION:
; APPLICANT: Kimoto, No. 6485948ihiro
; APPLICANT: Mitsuhashi, Kazuo
; TITLE OF INVENTION: NOVEL CARBONYL REDUCTASE, METHOD FOR PRODUCING SAID ENZYME, DNA
; TITLE OF INVENTION: ENCODING SAID ENZYME, AND METHOD FOR PRODUCING ALCOHOL USING SAID
; TITLE OF INVENTION: ENZYME
; FILE REFERENCE: 06501-050001
; CURRENT APPLICATION NUMBER: US/09/940,037A
; PRIOR FILING DATE: 2000-08-27
; PRIOR FILING DATE: 1999-12-21
; PRIOR FILING DATE: 1999-12-21
; PRIOR FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0, reformatted using WordPerfect 5.1
; SEQ ID NO 29
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-940-037A-29

Query Match      24.5%; Score 341.5; DB 4; Length 261;
Best Local Similarity 34.4%; Pred. No. 1.1e-28;
Matches 93; Conservative 50; Mismatches 98; Indels 29; Gaps 10;

Qy 11 LEGKVALITGGASGIGETTAKLFSOHGAKVAI---ADVQD--ELGHSVVEAIGTSNSTVI 65
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 5 LKGVVAITGAASGLGKAMAIRFGKEQAKVINYNSKQDPNEVKEEVIKAGG--EAVVV 62
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 66 HCDVTNEDGVKNVAVNTVSTYKLDIMFSNAGISDPNRPRIIDNEK--ADPERVLSVNT 123
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 63 QGDTVTEEDVKNIQVTAIKEFGTLDIMINNAGLENP---VPSHEMLPKDWDKVIQTNLT 118
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 124 GVFLCKMKAARVMIPAR-SGNIISTASISSTWGGSSHAYCGSKHVALATRLNLAVELGQ 182
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 119 GAFGLSREAIKYFVENDIKGNVINSSVHEVWPFLFVHYAASKGKIKMTETLALAYAP 178
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 183 FGIRVNCCLSPFLPTAL-CKKESGINKNEEPEENVINPAGNLKGPKNVEDVANAALYLAS 241
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
; US-09-134-001C-5042

Query Match      23.8%; Score 331.5; DB 4; Length 267;
Best Local Similarity 32.1%; Pred. No. 1.4e-27;
Matches 88; Conservative 55; Mismatches 96; Indels 35; Gaps 9;

Qy 11 LEGKVALITGGASGIGETTAKLFSOHGAKVAIADVQDELGHVSVEAIGTSNSTY----- 64
Db 9 LENKVVLIITGAATGIGKIAENFGKAKAVI-NVRSDRHHSEIEIEIKQTVAKFGGQTLA 67
Qy 65 IHCVDVTNEDGVKNVAVNTVSTYKLDIMFSNAGI--SDPNRPRIIDNEKADFERVLSVV 122
Db 68 VQGDVSIIEEDIKRMIEITLINHFGTLDIINNAGFENSIPTHEMSID---DWQKVIDINL 123
Qy 123 TGVFLCKMKAARVMIPAR-RSGNIISTASISSTWGGSSHAYCGSKHVALATRLNLAVELG 181
Db 124 TGAFGSRETINQFLKENKGTIINISSVHDTIPWPNVHYAASKGGLKMMETMSMEYA 183
Qy 182 QFGIRVNCCLSPFLPTALGK-KFSGIKNEEPEENVINPAGNLKGPK---FNVEDVANAAL 237
Db 184 QYGRINNIISPGAIIVTEHTKPKSDPTTREETIKMI-----PAREIGNAQDVANAVL 235
Qy 238 YLASDEAKYVSGHNLFIDGFSVCNSVIKFOYP 271
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 236 FLSSDLASYIHGTTLTYVDGG-----MMNYP 260
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Search completed: October 23, 2003, 12:52:01
Job time : 30 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 23, 2003, 12:50:44 ; Search time 68 Seconds  
(without alignments)  
672.305 Million cell updates/sec

Title: US-09-673-918A-2

Perfect score: 1393

Sequence: 1 MQLRTAFARLEGGKVALITG.....IDGFSVCNSVIKVFQVPS 273

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 629382 seqs, 167460630 residues

Total number of hits satisfying chosen parameters: 629382

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*

2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*

3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*

4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*

5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*

6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*

7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*

8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*

9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*

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11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*

12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*

13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*

14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*

15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*

16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*

17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description         |
|------------|-------|-------------|--------|-------|---------------------|
| 1          | 1233  | 88.5        | 276    | 10    | US-09-944-160-24    |
| 2          | 487.5 | 35.0        | 272    | 12    | US-10-242-574-82    |
| 3          | 432   | 31.0        | 253    | 9     | US-09-815-242-11842 |
| 4          | 382   | 27.4        | 258    | 15    | US-10-156-761-11335 |
| 5          | 380.5 | 27.3        | 263    | 15    | US-10-156-761-14255 |
| 6          | 369   | 26.5        | 256    | 10    | US-09-354-314-14    |
| 7          | 369   | 26.5        | 256    | 15    | US-10-230-562-14    |
| 8          | 349.5 | 25.1        | 262    | 9     | US-09-802-853-6     |
| 9          | 349.5 | 25.1        | 262    | 15    | US-10-307-385-6     |
| 10         | 343.5 | 24.7        | 267    | 10    | US-09-773-748-1     |
| 11         | 343.5 | 24.7        | 267    | 12    | US-10-327-726-1     |
| 12         | 341.5 | 24.5        | 261    | 10    | US-09-940-037A-29   |
| 13         | 332   | 23.8        | 245    | 12    | US-10-237-496-82    |
| 14         | 332   | 23.8        | 245    | 12    | US-10-242-074-82    |
| 15         | 332   | 23.8        | 245    | 12    | US-10-242-505-82    |

|    |     |      |     |    |                  |                   |
|----|-----|------|-----|----|------------------|-------------------|
| 16 | 332 | 23.8 | 245 | 12 | US-10-242-574-82 | Sequence 82, Appl |
| 17 | 332 | 23.8 | 245 | 12 | US-10-243-261-82 | Sequence 82, Appl |
| 18 | 332 | 23.8 | 245 | 12 | US-10-243-282-82 | Sequence 82, Appl |
| 19 | 332 | 23.8 | 245 | 12 | US-10-243-402-82 | Sequence 82, Appl |
| 20 | 332 | 23.8 | 245 | 12 | US-10-243-431-82 | Sequence 82, Appl |
| 21 | 332 | 23.8 | 245 | 12 | US-10-245-164-82 | Sequence 82, Appl |
| 22 | 332 | 23.8 | 245 | 12 | US-10-244-972-82 | Sequence 82, Appl |
| 23 | 332 | 23.8 | 245 | 12 | US-10-197-942-82 | Sequence 82, Appl |
| 24 | 332 | 23.8 | 245 | 12 | US-10-238-196-82 | Sequence 82, Appl |
| 25 | 332 | 23.8 | 245 | 12 | US-10-238-013-82 | Sequence 82, Appl |
| 26 | 332 | 23.8 | 245 | 15 | US-10-245-103-82 | Sequence 82, Appl |
| 27 | 332 | 23.8 | 245 | 15 | US-10-245-107-82 | Sequence 82, Appl |
| 28 | 332 | 23.8 | 245 | 15 | US-10-245-143-82 | Sequence 82, Appl |
| 29 | 332 | 23.8 | 245 | 15 | US-10-245-771-82 | Sequence 82, Appl |
| 30 | 332 | 23.8 | 245 | 15 | US-10-245-851-82 | Sequence 82, Appl |
| 31 | 332 | 23.8 | 245 | 15 | US-10-245-883-82 | Sequence 82, Appl |
| 32 | 332 | 23.8 | 245 | 15 | US-10-237-535-82 | Sequence 82, Appl |
| 33 | 332 | 23.8 | 245 | 15 | US-10-238-183-82 | Sequence 82, Appl |
| 34 | 332 | 23.8 | 245 | 15 | US-10-238-283-82 | Sequence 82, Appl |
| 35 | 332 | 23.8 | 245 | 15 | US-10-238-370-82 | Sequence 82, Appl |
| 36 | 332 | 23.8 | 245 | 15 | US-10-245-055-82 | Sequence 82, Appl |
| 37 | 332 | 23.8 | 245 | 15 | US-10-245-147-82 | Sequence 82, Appl |
| 38 | 332 | 23.8 | 245 | 15 | US-10-245-730-82 | Sequence 82, Appl |
| 39 | 332 | 23.8 | 245 | 15 | US-10-245-739-82 | Sequence 82, Appl |
| 40 | 332 | 23.8 | 245 | 15 | US-10-246-210-82 | Sequence 82, Appl |
| 41 | 332 | 23.8 | 245 | 15 | US-10-239-196-82 | Sequence 82, Appl |
| 42 | 332 | 23.8 | 245 | 15 | US-10-243-024-82 | Sequence 82, Appl |
| 43 | 332 | 23.8 | 245 | 15 | US-10-243-409-82 | Sequence 82, Appl |
| 44 | 332 | 23.8 | 245 | 15 | US-10-245-621-82 | Sequence 82, Appl |
| 45 | 332 | 23.8 | 245 | 15 | US-10-245-880-82 | Sequence 82, Appl |

ALIGNMENTS

RESULT 1

US-09-944-160-24  
; Sequence 24, Application US/09944160  
; Patent No. US20020174452A1  
; GENERAL INFORMATION:  
; APPLICANT: Lewis, No. US20020174452A1man  
; APPLICANT: .. Huang, Ning  
; TITLE OF INVENTION: Monocot Seeds with Increased Lignan  
; TITLE OF INVENTION: Content  
; FILE REFERENCE: WSUR117983  
; CURRENT APPLICATION NUMBER: US/09/944,160  
; PRIOR FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: US 60/230,632  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 276  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: secoisolaricresinol dehydrogenase amino acid  
; OTHER INFORMATION: sequence from plasmid pAPI249  
US-09-944-160-24

|                       |                  |                                                               |                |             |
|-----------------------|------------------|---------------------------------------------------------------|----------------|-------------|
| Query Match           | 88.5%            | Score 1233;                                                   | DB 10;         | Length 276; |
| Best Local Similarity | 88.2%;           | Pred. No. 3.7e-115;                                           | Mismatches 18; | Indels 0;   |
| Matches 240;          | Conservative 14; |                                                               |                | Gaps 0;     |
| Qy                    | 2                | QLRTAFARLEGGKVALITGASGIGETTAKLFQHGAKVAIADVDLGHVSVEAIGTSN      | 61             |             |
| Db                    | 5                | QLRTAFARLEGGKVALITGASGIGETTAKLFQHGAKVAIADVDLGHVSVEAIGLSN      | 64             |             |
| Qy                    | 62               | STVHCDDVTNEDGVKNAVDNTVSTYKGLDIFMNFNAGISDPNRPRIIDNEKADFERVLSVN | 121            |             |
| Db                    | 65               | STVHCDDVTNEDGVKNAVDNTVSTYKGLDIFMNFNAGISDPYKPRVIDNEKADFERVLSVN | 124            |             |

QY 122 VTGFLCMKHAARVMIPARSGNIISTASLSSTMGSSSHAYCGSKHAVLALTRNLAVEIG 181  
Db 125 VTGFLCMKHAARVMIPARSGNIISTASLSSTMGSSSHAYCGSKHAVLALTRNLAVEIG 184  
QY 182 QGIRVNCISPPGLPTALGKFKFSIGKNEEFENVINPAGNLKPKENVEDVANAALYLAS 241  
Db 185 QGIRVNCISPPGLPTALGKFKFSIGKNEEFENVINPAGNLKPKENVEDVANAALYLAS 244  
QY 242 DEAKVVSQNLFDGGSFVCSNKLKQYFDS 273  
Db 245 DEAKVVSQNLFDGGSFVCSNKLKQYFDS 276

## RESULT 2

US-10-342-224-8  
; Sequence 8, Application US/10342224  
; Publication No. US20030162294A1  
; GENERAL INFORMATION:  
; APPLICANT: Nathalie Verbruggen  
; TITLE OF INVENTION: Genes Involved in Tolerance to Environmental Stress  
; FILE REFERENCE: CNN-012US  
; CURRENT APPLICATION NUMBER: US/10/342,224  
; CURRENT FILING DATE: 2003-01-13  
; PRIOR APPLICATION NUMBER: US/09/762,154  
; PRIOR FILING DATE: 2002-02-02  
; PRIOR APPLICATION NUMBER: EP 98202634.6  
; PRIOR FILING DATE: 1998-08-04  
; NUMBER OF SEQ ID NOS: 123  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 272  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-342-224-8

Query Match 35.0%; Score 487.5; DB 12; Length 272;  
Best Local Similarity 44.2%; Pred. No. 1.6e-40;  
Matches 118; Conservative 45; Mismatches 91; Indels 13; Gaps 7;  
QY 9 RRLGKVALITGGASIGGETTAKLFSQHGAKVAIADVDDELGHVSVEAI--GTSNSTVI 68  
Db 6 KRLFEKVAITGGARGIGAAITLFTENGAYVIVADILNDELGLVAESIG--GCYVHCD 62  
QY 69 VTNEDGVKNADVNTVSTYKLDIMFSNAGISDPNRPRIIDNEKADPERVLSVNVTVGFLC 128  
Db 63 VSKEADVEAAVELAMRRKGRLDVNFNAGMS-LNEGSIMGMDVDMVKNLVSNNVNGVLHG 121  
QY 129 MKHAARVMIP-ARSGNIISTASLSSTMGSSSHAYCGSKHAVLALTRNLAVEIGQFGIRV 187  
Db 122 IKHAAMIKGGRGSGIITCTSSSGLMGLGCHAYTILSKGNGVVRVTTCELGSHGIRV 181  
QY 188 NCLSPFGLPT----ALGKFKSGIK-NEEFENVINPAGN-LKPKENVEDVANAALYL 240  
Db 182 NSISPHGVPTDILVNAYRKFLNNDKLVNAEVTDIIAEKGSLITGRAGTVEDVAQAALFLA 241  
QY 241 SDEAK-YVSGHNLFDGGSFVCSNKLKQYFDS 266  
Db 242 SQESSGFIITHNLVVDGGYTSATSMR 268

## RESULT 3

US-09-815-242-11842  
; Sequence 11842, Application US/09815242  
; Patent No. US2002061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haseibeck, Robert  
; APPLICANT: Ohlsen, Karl L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11842  
; LENGTH: 253  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-815-242-11842

Query Match 31.0%; Score 432; DB 9; Length 253;  
Best Local Similarity 37.5%; Pred. No. 5.2e-35;  
Matches 95; Conservative 52; Mismatches 98; Indels 8; Gaps 4;  
QY 8 ARRLGKVALITGGASIGGETTAKLFSQHGAKVAIADVDDELGHVSVEAI--GTSNSTVI 65  
Db 2 SKLLSGQVALYTGGAAGIGRATALAFAAAGVKVVVADLDSAGGEGTVEAIROAGGEALFI 61  
QY 66 HDVTNEDGVKNADVNTVSTYKLDIMFSNAGISDPNRPRIIDNEKADPERVLSVNVTVG 125  
Db 62 RCDVTRDAEVAALVEGCAAYGRLDYAFNNAGI--EIEQKLADNAGEEPDAIWNVVKGV 120  
QY 126 FLCKMKAARVMIPARSGNIISTASLSSTMGSSSHAYCGSKHAVLALTRNLAVEIGQFGI 185  
Db 121 WLCMKHQIPLMLQAQGGGAIVNTASVAGLGAAPKMSIYAASKHAVIGLTKSAALYAKKGI 180  
QY 186 RVNCLSPFGLPTALGK-K-FSGIKNEEFENVINPAGNLKPKENVEDVANAALYLASDEA 244  
Db 181 RVNAVCPAVIDTDMFRAYEADPRKAEFAAAMHPLGRVG----RVBEIAAAVLYLCCDNA 236  
QY 245 KYVSGHNLFDGG 257  
Db 237 GFTTGIALPVDGG 249

## RESULT 4

US-10-156-761-11335  
; Sequence 11335, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109

```
; SEQ ID NO 11335
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-11335

Query Match      27.4%; Score 382; DB 15; Length 258;
Best Local Similarity 36.8%; Pred. No. 5.4e-30;
Matches 96; Conservative 46; Mismatches 109; Indels 10; Gaps 4;

Qy 10 RLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSNITYHCDV 69
Db 3 KLDGRVLLISGAARGQEQEARLVEBGAQVVAADVLDDQGEALAKEIG---ARYVHLDV 59
Qy 70 TNEGVKNVNDVTSTYCKLIDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTVGVFLCM 129
Db 60 GREDDWQAQAVTVAKDAYGHIDGLVNNAGILRPN--DLVGTPLAEFQOIVQVQGVFLGI 117
Qy 130 KHAARVMIPARSGNIISTASLSSTWGGSSHAYCGSKHAVLALTRNLAVELGQFGIRWC 189
Db 118 KTVAPEIEAAGGGTIVNTASVAGLTGMAYYGAYTATKHAIVGLTRVAALAEAAKKIRVNA 177
Qy 190 LSPGLTALCKKFS---GKNEEFENFVNFAGNL--KGPKNVEDVANAALYLASDEA 244
Db 178 VCPGAIIDTAMSNPSQLDPGADPEETARALSSELYGRVLPGLGRIPRPEEVARLALFLSGEDS 237
Qy 245 KYVSGHNLFDIDGGFSCNVI 265
Db 238 SYITGQPFVIDGGWLAGVSVI 258

RESULT 5
US-10-156-761-14255
; Sequence 14255, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 14255
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-14255

Query Match      27.3%; Score 380.5; DB 15; Length 263;
Best Local Similarity 35.3%; Pred. No. 7.9e-30;
Matches 89; Conservative 48; Mismatches 108; Indels 7; Gaps 3;

Qy 9 RLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSNITYHCD 68
Db 11 RRLVGRVAVITGAGSGIGLATARELSAGHVCGDIDEVSGKAAAEVGG---GTFVQVD 67
Qy 69 VTNEGVKNVNDVTSTYCKLIDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTVGVFLC 128
Db 68 VTDAEQEALERTAYDYGSVDIAFNAGISFPDDDSILETGLEAWKRVQEVNLTSVLC 127
Qy 129 MKHAARVMIPARSGNIISTASLSSTWGGSSH-AYCGSKHAVLALTRNLAVELGQFGIRV 187
Db 128 CKAALPYMRQGRGSIINTASVFMGAATSQISYTASKGGLAWSRELGVQFPAREGIRV 187
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Qy 188 NCLSPFGLPTALGKFKSGIKNEEEFENFVNFAGNLKGPKNVEDVANAALYLASDEAKYV 247
Db 188 NALCPGPNVTPLLQELFPAKDPERAAARLHVIP---VGRFAEAEIAAAVAFLASDDSSFV 244
Qy 248 SGHNLFDIDGGFS 259
Db 245 NATDFLVDGGIS 256

RESULT 6
US-09-954-314-14
; Sequence 14, Application US/09954314
; Patent No. US20020127666A1
; GENERAL INFORMATION:
; APPLICANT: Rouviere, Pierre E.
; APPLICANT: Brzostowicz, Patricia C.
; TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIATES
; FILE REFERENCE: BC1001 US NA
; CURRENT APPLICATION NUMBER: US/09/954,314
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/120,702
; PRIOR FILING DATE: 1999-February-19
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 14
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Brevibacterium ep HCU
US-09-954-314-14

Query Match      26.5%; Score 369; DB 10; Length 256;
Best Local Similarity 35.7%; Pred. No. 1.1e-28;
Matches 91; Conservative 55; Mismatches 101; Indels 8; Gaps 5;

Qy 10 RLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSN--STYIHC 67
Db 3 RLGGKVAIVTGGAAAGMGRISQSELYASEGAQVAVVDVNEQEGRATADAIRASGGVANYWKL 62
Qy 68 DVTNEGVKNVNDVTSTYCKLIDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTVGVFL 127
Db 63 DVSDSESEIVVSDIAKRFAGINVLVNNAGVTGADKPTHEIDER-DLDLVLSDVDKGVFF 121
Qy 128 CMKHAARVMIPARSGNIISTASLSSTWGGSSHAYCGSKHAVLALTRNLAVELGQFGIRV 187
Db 122 MTKHCIPYFKQAGGAIWVFASIVGLVGSQELTPYHAAKGAVALTKQDATTYGPSNIRV 181
Qy 188 NCLSPFGLPTALGKFKSGIKNEEEFENFVNFAGNLKGPKNV---EDVANAALYLASDEA 244
Db 182 NAVAPGTILTPVLKEL--GSRGPDLDGYTKLMG-AKHPGLGRVGTPEEVAATFLASEEA 239
Qy 245 KYVSGHNLFDIDGGFS 259
Db 240 SFTIGAVLPVDGGYT 254
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```
RESULT 7
US-10-230-562-14
; Sequence 14, Application US/10230562
; Publication No. US20030113886A1
; GENERAL INFORMATION:
; APPLICANT: Rouviere, Pierre E.
; APPLICANT: Brzostowicz, Patricia C.
; TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID
; TITLE OF INVENTION: INTERMEDIATES
; FILE REFERENCE: BC-1001
; CURRENT APPLICATION NUMBER: US/10/230,562
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/120,702
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 14
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; LENGTH: 256
; TYPE: PRT
; ORGANISM: Brevibacterium sp HCU
US-10-230-562-14

Query Match      26.5%; Score 369; DB 15; Length 256;
Best Local Similarity 35.7%; Pred. No. 1.1e-28;
Matches 91; Conservative 55; Mismatches 101; Indels 8; Gaps 5;

Qy 10 RLEGKVALITGASGIGETTAKLFSQHGAKVAIADVQDELGHVSVEAIGTSN--STYIHC 67
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 3 RLGGKVAVITGGAAGMGRITQSEYASGAQVAVVDVNEQEGRATADAIRASGGVANYWKL 62
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 68 DVTNEDGVKNVADNTVSTYTKLIDMFSNAGISDPNRIIDNEKADPERVLSVNVTVGVEL 127
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 63 DVSDESEIVEIVSDIAKRFAGINLVNNAAGVTGADKPTHEIDER-DLDVLVSDVKGVEF 121
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 128 CMKHAARVMIPARSGNIISTASLSMTGGSSHAYCGSKHVALTRNLAVELQGFQIRV 187
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 122 MYGHCIPYEQAGGGAIVNFASIVGLVGSQELTPYHAAKGAVALTKQDAVTYGPSNIRV 181
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 188 NCLSPFGLTALGKFKSGIKNEEFENFVINFAGNLKGPKNV---EDVANAALYLASDEA 244
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 182 NAVAPOTILTPVLKEL-GSRGPDGLDGYTKLMG-AKHPLGRVGTPEEVAATLFLASEEA 239
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 245 KYVSGHNLFDGGFS 259
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 240 SFITGAVLPVDGGYT 254
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 8
US-09-802-853-6
; Sequence 6, Application US/09802853
; Patent No. US20010034049A1
; GENERAL INFORMATION:
; APPLICANT: SUGIYAMA, MASAKAZU
; APPLICANT: TONOUCHI, NAOTO
; APPLICANT: SUZUKI, SHUNICHI
; APPLICANT: YOKOZEKI, KENZO
; TITLE OF INVENTION: XYLIOTOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF
; FILE REFERENCE: 0010-1024-0
; CURRENT APPLICATION NUMBER: US/09/802,853
; PRIOR FILING DATE: 2001-03-12
; PRIOR FILING DATE: 1999-07-29
; PRIOR FILING DATE: 1999-07-29
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Gluconobacter oxydans
US-09-802-853-6

Query Match      25.1%; Score 349.5; DB 9; Length 262;
Best Local Similarity 31.2%; Pred. No. 9.9e-27;
Matches 83; Conservative 55; Mismatches 107; Indels 21; Gaps 6;

Qy 8 ARLEGKVALITGASGIGETTAKLFSQHGAKVAIADVQDEL---GHSVVEAIGTSNSTY 64
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 2 SKFNGKVLVTGAGNIGLATALRLAEGTAIALLDMNREALEKASVREKGVARSY 61
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 65 IHCVDVNEGVKNVADNTVSTYTKLIDMFSNAGISDPNRIIDNEKADPERVLSVNVTVG 124
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 62 V-CDVTSSEAVIGTVDSVVRDFGKIDFLFNNAAGYQGAFAF-VQDYPSSDDFARVLITNV 119
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 125 VFLCMKHAARVMIPARSGNIISTASLSMTGGSSHAYCGSKHVALTRNLAVELQGFQ 184
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 120 AFHVLKAVSRQMTQNYGRIVNTASMGVKKPPNMAAYGASKGAIITALTETAALDLAPYN 179
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 185 IRVNCCLSP-----FGLPTALGKFKSGIKNEEFENFVINFAGNLKGPKNV-NVED 231
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 180 IRVNAISPGYMGPGFMWRQVELQAKVGSQVFPSTDPKVAQOMI---GSPVPMRRYGDINE 236
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

US-09-802-853-6
Query Match      25.1%; Score 349.5; DB 15; Length 262;
Best Local Similarity 31.2%; Pred. No. 9.9e-27;
Matches 83; Conservative 55; Mismatches 107; Indels 21; Gaps 6;

Qy 8 ARLEGKVALITGASGIGETTAKLFSQHGAKVAIADVQDEL---GHSVVEAIGTSNSTY 64
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 2 SKFNGKVLVTGAGNIGLATALRLAEGTAIALLDMNREALEKASVREKGVARSY 61
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 65 IHCVDVNEGVKNVADNTVSTYTKLIDMFSNAGISDPNRIIDNEKADPERVLSVNVTVG 124
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 62 V-CDVTSSEAVIGTVDSVVRDFGKIDFLFNNAAGYQGAFAF-VQDYPSSDDFARVLITNV 119
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 125 VFLCMKHAARVMIPARSGNIISTASLSMTGGSSHAYCGSKHVALTRNLAVELQGFQ 184
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 120 AFHVLKAVSRQMTQNYGRIVNTASMGVKKPPNMAAYGASKGAIITALTETAALDLAPYN 179
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 185 IRVNCCLSP-----FGLPTALGKFKSGIKNEEFENFVINFAGNLKGPKNV-NVED 231
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 180 IRVNAISPGYMGPGFMWRQVELQAKVGSQVFPSTDPKVAQOMI---GSPVPMRRYGDINE 236
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

US-09-773-748-1
; Sequence 1, Application US/09773748
; Publication No. US20020187537A1
; GENERAL INFORMATION:
; APPLICANT: Wada, Masaru
; TITLE OF INVENTION: Levodione reductase gene and use thereof
; FILE REFERENCE: Levodione reductase
; CURRENT APPLICATION NUMBER: US/09/773,748
; PRIOR FILING DATE: 2001-01-31
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 267
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FILE REFERENCE: P3630R1C4  
CURRENT APPLICATION NUMBER: US/10/237.496  
CURRENT FILING DATE: 2002-09-06  
PRIOR APPLICATION NUMBER: 10/197942  
PRIOR FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 60/059114  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/065027  
PRIOR FILING DATE: 1997-11-10  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/086478  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090689  
PRIOR FILING DATE: 1998-06-25  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 116  
SEQ ID NO 82  
LENGTH: 245  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-237-496-82

Query Match 23.8%; Score 332; DB 12; Length 245;  
Best Local Similarity 33.5%; Pred. No. 5.1e-25;  
Matches 85; Conservative 57; Mismatches 98; Indels 14; Gaps 7;  
Qy 10 RUEGKVALITGASIGETTAKLFSQHGAKVAIADVODELGHVSVEAIGTSNHYHCDV 69  
Db 3 RLDGKVIILTAQAQIGQAALAFAREGAKVIATDINESKQLSEKYPGIGQTRV---LDV 59  
Qy 70 TNEGDKVNAVNTYSTYKGLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTVGLCM 129  
Db 60 TK----KKQIDQFASEVERLDVLENAVGF--VHHGTVDLCEEDKDFSMNLNVRSMYLM 113  
Qy 130 KHAARVMIPARSNGIISTASLSSTMTGGSSH-AYCGSKHVALALTRNLAVELGQFGIRVN 188  
Db 114 KAPLPKMLAQKSGNIINSSVASSVKGVNRCVYSTTKAAVIGLTKSLAADFTQQGIRCN 173  
Qy 189 CLSPFGLPT-ALGKKFSGIKNEEFENVINPAGNLKGPKE-NVEDVANAALYLASDEAKY 246  
Db 174 CVCPGTVDTPSLQERIQARGNPEARN--DFLKKQKTGRFATAEETIAMLCVYLASDESAY 231  
Qy 247 VSGHNLFDGGFSV 260  
Db 232 VTGNPVIIDGGWSL 245

RESULT 14  
US-10-242-074-82  
Sequence 82, Application US/10242074  
Publication No. US20030138897A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin  
APPLICANT: Eaton, Dan  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe  
APPLICANT: Watande, Colin  
APPLICANT: Zhang, Zemin  
APPLICANT: Fong, Sherman

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3630R1C19  
CURRENT APPLICATION NUMBER: US/10/242.074  
CURRENT FILING DATE: 2002-09-11  
PRIOR APPLICATION NUMBER: 10/197942  
PRIOR FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 60/059114  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/065027  
PRIOR FILING DATE: 1997-11-10  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/086478  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090689  
PRIOR FILING DATE: 1998-06-25  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 116  
SEQ ID NO 82  
LENGTH: 245  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-242-074-82

Query Match 23.8%; Score 332; DB 12; Length 245;  
Best Local Similarity 33.5%; Pred. No. 5.1e-25;  
Matches 85; Conservative 57; Mismatches 98; Indels 14; Gaps 7;  
Qy 10 RUEGKVALITGASIGETTAKLFSQHGAKVAIADVODELGHVSVEAIGTSNHYHCDV 69  
Db 3 RLDGKVIILTAQAQIGQAALAFAREGAKVIATDINESKQLSEKYPGIGQTRV---LDV 59  
Qy 70 TNEGDKVNAVNTYSTYKGLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTVGLCM 129  
Db 60 TK----KKQIDQFASEVERLDVLENAVGF--VHHGTVDLCEEDKDFSMNLNVRSMYLM 113  
Qy 130 KHAARVMIPARSNGIISTASLSSTMTGGSSH-AYCGSKHVALALTRNLAVELGQFGIRVN 188  
Db 114 KAPLPKMLAQKSGNIINSSVASSVKGVNRCVYSTTKAAVIGLTKSLAADFTQQGIRCN 173  
Qy 189 CLSPFGLPT-ALGKKFSGIKNEEFENVINPAGNLKGPKE-NVEDVANAALYLASDEAKY 246  
Db 174 CVCPGTVDTPSLQERIQARGNPEARN--DFLKKQKTGRFATAEETIAMLCVYLASDESAY 231  
Qy 247 VSGHNLFDGGFSV 260  
Db 232 VTGNPVIIDGGWSL 245

RESULT 15  
US-10-242-505-82  
Sequence 82, Application US/10242505  
Publication No. US20030138898A1  
GENERAL INFORMATION:  
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APPLICANT: Wood, William

APPLICANT: Zhang,Zemin  
APPLICANT: Fong,Sherman  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3630R1C25  
CURRENT APPLICATION NUMBER: US/10/242,505  
CURRENT FILING DATE: 2002-09-11  
PRIOR APPLICATION NUMBER: 10/197942  
PRIOR FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 60/059114  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/065027  
PRIOR FILING DATE: 1997-11-10  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/086478  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090689  
PRIOR FILING DATE: 1998-06-25  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 116  
SEQ ID NO 82  
LENGTH: 245  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-242-505-82

Query Match 23.8%; Score 332; DB 12; Length 245;  
Best Local Similarity 33.5%; Pred. No. 5.1e-25;  
Matches 85; Conservative 57; Mismatches 98; Indels 14; Gaps 7;

Qy 10 RLEGKVALITGGAGIGETTAKLFSOHGAKVAIADVODELGHSVVEAIGTSNSTYIHCDV 69  
Db 3 RLDGKVIILTRAAQIGQAALAFAREGAKVIATDINESKLOELEKYPGIQTRV---LDV 59

Qy 70 TNEDGVKNADVNTSTYKGLDIFSNAGISDPNRPRIIDNEKADFERVLSVNVTVGVFLCM 129  
Db 60 TK---KKQIQFASEVERLDVLFNVAGF--VHHGTVLDCCEKDWDFSMNLNVSWMYIMI 113

Qy 130 KHAARVMTPARSGNIISTASLSSTWGGSSH-AYCGSKHAVLALTRNLAVELQGFGRVN 188  
Db 114 KAFLPKMLAOKSGNIINMSSVASSVGVVNRVCVYSTTKAAVIGLTKSLAADFIQGGIRCN 173

Qy 189 CLSPFGLPT-ALGKKFSGIKNEEFENVINFAGNLKPKF-NVEDVANAALYLASDEAKY 246  
Db 174 CVCGTVDTPSLQRIQARGNPEARN--DFLKRQKTGRFATABEIAMLCVYLASDESAY 231

Qy 247 VSGHNLFTDGGFSV 260  
Db 232 VTGNPVIIDGGWSL 245

Search completed: October 23, 2003, 13:00:39  
Job time : 69 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 23, 2003, 12:45:39 ; Search time 40 Seconds  
(without alignments)  
656.351 Million cell updates/sec

Title: US-09-673-918a-2

Perfect score: 1393

Sequence: 1 MQLRTAPARLEKVALITG.....IDGGFSVCNSVIKVFQYFDS 273

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_76.\*

1: PIR1.\*

2: PIR2.\*

3: PIR3.\*

4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 734   | 52.7        | 267    | 2     | T11579      |
| 2          | 685   | 49.2        | 284    | 2     | T02257      |
| 3          | 658.5 | 47.3        | 285    | 2     | P96533      |
| 4          | 625.5 | 44.9        | 303    | 2     | T46084      |
| 5          | 597.5 | 42.9        | 283    | 2     | H85039      |
| 6          | 588.5 | 42.2        | 336    | 2     | A47542      |
| 7          | 575.5 | 41.3        | 264    | 2     | T02174      |
| 8          | 567   | 40.7        | 257    | 2     | T02175      |
| 9          | 559   | 40.1        | 251    | 2     | T06384      |
| 10         | 549.5 | 39.4        | 258    | 2     | T02176      |
| 11         | 499.5 | 35.9        | 234    | 2     | T03734      |
| 12         | 490.5 | 35.2        | 272    | 2     | T47354      |
| 13         | 432   | 31.0        | 253    | 2     | P83440      |
| 14         | 402.5 | 28.9        | 258    | 2     | C70885      |
| 15         | 398   | 28.6        | 256    | 2     | A10406      |
| 16         | 396   | 28.4        | 255    | 1     | S39737      |
| 17         | 386   | 27.7        | 255    | 2     | G82644      |
| 18         | 381.5 | 27.4        | 256    | 2     | E72427      |
| 19         | 370.5 | 26.6        | 260    | 2     | T36846      |
| 20         | 366   | 26.3        | 260    | 2     | H70758      |
| 21         | 363   | 26.1        | 246    | 2     | H72219      |
| 22         | 363   | 26.1        | 254    | 2     | A1478       |
| 23         | 363   | 26.1        | 254    | 2     | A11117      |
| 24         | 361.5 | 26.0        | 296    | 2     | E87260      |
| 25         | 357   | 25.6        | 248    | 2     | H86527      |
| 26         | 357   | 25.6        | 248    | 2     | D72036      |
| 27         | 356.5 | 25.6        | 243    | 2     | F83838      |
| 28         | 356   | 25.6        | 246    | 2     | H84136      |
| 29         | 353.5 | 25.4        | 286    | 2     | F91082      |

#### ALIGNMENTS

##### RESULT 1

T11579

Probable short chain alcohol dehydrogenase CPRD12, drought-inducible - cowpea  
C/Species: Vigna unguiculata (cowpea)  
C/Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 20-Jun-2000  
C/Accession: T11579

R/Iuchi, S.; Yamaguchi-Shinozaki, K.; Urao, T.; Shinozaki, K.

J. Plant Res. 109, 415-424, 1996

A/Title: Characterization of two cDNAs for novel drought-inducible genes in the highly d

A/Reference number: Z17293

A/Accession: T11579

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-267 <IUC>

A/Cross-references: EMBL:D88121

C/Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 52.7%; Score 734; DB 2; Length 267;

Best Local Similarity 56.3%; Pred. No. 8.1e-51;

Matches 147; Conservative 41; Mismatches 67; Indels 6; Gaps 2;

|    |     |                                                                   |
|----|-----|-------------------------------------------------------------------|
| Qy | 9   | RRLEGVALLTGASGIGETTAKLFSQHGAKVAIADVQDELHGSVVVEAIGTSNSTYTHCD 68    |
| Db | 12  | KRLGKVAIITGASGIGETARLFSQGHAVHVADIQDDVGLSLCNEL--KSAIVVHCD 69       |
| Qy | 69  | VTNEDGVKNADVNTVSTYKLDIMPSNAGISDPRRIIDNEKADPERVLSVNVTVGYFLC 128    |
| Db | 70  | VTKEEDIEKCVDTAVSKFGKLDIMFNAGTGDEFKKSILDNTKSDPERVLSVNLVGPFLG 129   |
| Qy | 129 | MKHAARVMIPARSGNIITASLSSTMTGGSSHAYCGSKHVALALTRNLAVELGQFGIRVN 188   |
| Db | 130 | TKHAARVMIPARKGCIINTASVAGCIGGGHATHATYTSKHALVGLTKNTAVELGQFGIRVN 189 |
| Qy | 189 | CLSPFFGLPTALGKFKSGINEEFENVINPAGNLKGFKNVEDVANAAALYLASDEAKYVS 248   |
| Db | 190 | CVSPFAIVTELLNKYNFLNDEGVKTYMNLKGVYVPV---NDVAEALYLASDESKEFVS 245    |
| Qy | 249 | GHNLFTDGGFSVCNSVIKVFQ 269                                         |
| Db | 246 | SHNLVIDGGLINSNVGPPMFE 266                                         |

##### RESULT 2

T02257

Probable short chain alcohol dehydrogenase - common tobacco  
C/Species: Nicotiana tabacum (common tobacco)

C/Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 21-Jul-2000

C/Accession: T02257

R/Herbers, K.; Moenke, G.; Badur, R.; Sonnewald, U.

Plant Mol. Biol. 29, 1027-1038, 1995

A/Title: A simplified procedure for the subtractive cDNA cloning of photoassimilate-resp

A/Reference number: S62698; MUID:96145513; PMID:8555446











C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
 C/Accession: C70885  
 R/Col: S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 399, 537-544, 1998  
 A/Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrall, B.G.  
 A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
 A/Reference number: A70500; MUID:198295987; PMID:9634230  
 A/Accession: C70885  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-258 <COL>  
 A/Cross-references: GB:AL008883; GB:AL123456; NID:G3261490; PIDN:CAA15519.1; PID:G261280  
 A/Experimental source: strain H37RV  
 C/Genetics:  
 A/Gene: Rv2857c  
 C/Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology  
 F;11-188/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 28.9%; Score 402.5; DB 2; Length 258;  
 Best Local Similarity 35.8%; Pred. No. 1.5e-24;  
 Matches 91; Conservative 49; Mismatches 105; Indels 9; Gaps 4;

Qy 8 ARLEKGVALLTGAGSGICETTKLFSQHGAQVAIADVDDELGHVSUVEAIGTSNSTYIHC 67  
 Db 5 SQRLAGRVAVITGGSGIGLAGRMRAGATIVGDDVDEAGGADEL---SGLFVPT 61  
 Qy 68 DVTNEDGVKNVNDVNTVSTYKGLDIFMSNAGISDPNRPRIIDNEKADFERVLSVNTGVFL 127  
 Db 62 DVCEDEAVNGLPDAETVGRIDIAFNAGISPPEDNLIENIELAAWRQVDVNLKSVYL 121  
 Qy 128 CMKHAARVMPARSGNIISTASLSSTMGSGSHAYCGSKHAYLALTRNLAVELGQFGIR 186  
 Db 122 CCRAALRHVMVLAKGSIIVNTAFVAVMGSAISQISYTASKGVILAMRELGVQFARQGI 181  
 Qy 187 VNCLSPFGLPTALGKFKGKNEEFENVINP-AGNLKGPKEFVEDVANAALYLASDEAK 245  
 Db 182 VNALCFGPVNTPLQLFLFARNPERAARMVHVLGRFAEP---DEIAAAVAFILASDDAS 237  
 Qy 246 YVSGHNLFDGGFS 259  
 Db 238 FITASTFLVDGGIS 251

RESULT 15  
 A10406  
 Probable dehydrogenase YPO3351 [imported] - Yersinia pestis (strain CO92)  
 C/Species: Yersinia pestis  
 C/Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Nov-2001  
 C/Accession: A10406  
 R/Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; Geno-Taraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Li, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, Nature 413, 523-527, 2001  
 A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
 A/Reference number: AB0001; MUID:21470413; PMID:11586360  
 A/Accession: A10406  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-256 <KUR>  
 A/Cross-references: GB:AL590842; PIDN:CAC92581.1; PID:G15981278; GSPDB:GN00175  
 C/Genetics:  
 A/Gene: YPO3351  
 C/Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 28.6%; Score 398; DB 2; Length 256;  
 Best Local Similarity 37.4%; Pred. No. 3.4e-24;  
 Matches 99; Conservative 51; Mismatches 87; Indels 28; Gaps 9;

Qy 5 TAFARLEGKVALITGASGIGETTKLFSQHGAQVAIADVDDELGHVSUVEAIGTSNSTY 64  
 Db 10 TAFS--LSGKVAITGGATGIGHAELYLAKGARVLMDCADNVA-EIAQLDRDNVAG 66

Qy 65 IHCDVTNEDGVKNVNDVNTVSTYKGLDIFMSNAGIS--DNRPRIIDNEKA---DFERVLS 119  
 Db 67 LHCDVSDSQSVRQVAQAICATGQLDILVNSAGIAALDP-----AEKVREQDWDRITD 119  
 Qy 120 VNYTGVFLCMKHAARVMPARSGNIISTASLSSTMGSGSHAYCGSKHAYLALTRNLAVE 179  
 Db 120 INLKGVFLMCQEVGKHFIQHGKIVNLASQAGVVALPNHILAYCASKFGVIGITKVLALE 179  
 Qy 180 LGQFGIRVNCCLSPFGLPTALGKK-ESGKNEEFENVINPAGNLKGP--KENV-EDVANA 235  
 Db 180 WGPLDIQVNAISTVTVITLALGQKAWSGQLAEDM-----KLKIPARRFAYPAEVAAC 230  
 Qy 236 ALYLASDEAKYVSGHNLFDGGFSV 260  
 Db 231 ALFLASDAANMITGENLVIDGGYTI 255

Search completed: October 23, 2003, 12:51:25  
 Job time : 42 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 23, 2003, 12:38:34 ; Search time 23 Seconds  
(without alignments)  
558.187 Million cell updates/sec

Title: US-09-673-918A-2

Perfect score: 1393

Sequence: 1 MQLRTAFARRLEKGVALLTG.....IDGFGSVCSNVIKVFQYDPS 273

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 588.5 | 42.2        | 336    | 1  | TS2 MAIZE   |
| 2          | 406   | 29.1        | 250    | 1  | LINC_PSEPA  |
| 3          | 396   | 28.4        | 255    | 1  | YMPD_BACSU  |
| 4          | 381.5 | 27.4        | 256    | 1  | Y019_THEMA  |
| 5          | 376   | 27.0        | 250    | 1  | LINC_PSEPA  |
| 6          | 366   | 26.3        | 260    | 1  | YK02_MYCTU  |
| 7          | 363   | 26.1        | 246    | 1  | FABG_THEMA  |
| 8          | 357   | 25.6        | 248    | 1  | FABG_CHLNU  |
| 9          | 346   | 24.8        | 251    | 1  | Y325_THEMA  |
| 10         | 345.5 | 24.8        | 261    | 1  | YGVW_ECOLI  |
| 11         | 343.5 | 24.7        | 267    | 1  | LVR_LEIAO   |
| 12         | 341.5 | 24.5        | 261    | 1  | DHG_BACSU   |
| 13         | 334   | 24.0        | 253    | 1  | YAMP_RHISN  |
| 14         | 332.5 | 23.9        | 248    | 1  | FABG_CHLNU  |
| 15         | 332   | 23.8        | 263    | 1  | UCPA_SALTY  |
| 16         | 329.5 | 23.7        | 277    | 1  | LINC_RHOSH  |
| 17         | 328.5 | 23.6        | 256    | 1  | DHSD_RHOSH  |
| 18         | 326.5 | 23.4        | 247    | 1  | FABG_CHLTR  |
| 19         | 320.5 | 23.0        | 244    | 1  | FABG_VIBCH  |
| 20         | 320.5 | 23.0        | 262    | 1  | YBHD_BACSU  |
| 21         | 320   | 23.0        | 255    | 1  | 2BHD_STREX  |
| 22         | 316.5 | 22.7        | 244    | 1  | FABG_ECOLI  |
| 23         | 315.5 | 22.6        | 261    | 1  | DHG_BACME   |
| 24         | 315   | 22.6        | 270    | 1  | DHMA_FLAS1  |
| 25         | 314.5 | 22.6        | 261    | 1  | DHGI_BACME  |
| 26         | 313.5 | 22.5        | 241    | 1  | FABG_RICPR  |
| 27         | 310   | 22.3        | 263    | 1  | UCPA_ECO57  |
| 28         | 310   | 22.3        | 263    | 1  | UCPA_ECOLI  |
| 29         | 309.5 | 22.2        | 261    | 1  | DHGA_BACME  |
| 30         | 308.5 | 22.1        | 244    | 1  | FABG_SALTY  |
| 31         | 308.5 | 22.1        | 261    | 1  | DHG2_BACME  |
| 32         | 308   | 22.1        | 261    | 1  | DHBA_BACSU  |
| 33         | 307.5 | 22.1        | 244    | 1  | FABG_VIBHA  |

34 306.5 22.0 261 1 DHG3\_BACME  
35 306.5 22.0 261 1 DHG4\_BACME  
36 305.5 21.9 246 1 FABG\_BACSU  
37 305 21.9 255 1 YV06\_PSEAE  
38 303 21.8 255 1 HDHA\_ECOLI  
39 302 21.7 257 1 YXJF\_BACSU  
40 301 21.6 264 1 STCU\_EMENI  
41 300 21.5 249 1 BA71\_EUBSP  
42 296 21.2 262 1 DHGB\_BACME  
43 295.5 21.2 247 1 FAG1\_SYNV3  
44 295 21.2 249 1 BA72\_EUBSP  
45 293 21.0 256 1 GNO\_GLUOX

#### ALIGNMENTS

RESULT 1  
TS2\_MAIZE  
ID TS2\_MAIZE STANDARD; PRT; 336 AA.  
AC P50160;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Sex determination protein tasselseed 2.  
GN TS2.  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. W22;  
RX MEDLINE=93364991; PubMed=8358795;  
RA Delong A., Calderon-Urrea A., Dellaporta S.L.;  
RT "Sex determination gene TASSELSEED2 of maize encodes a short-chain  
RT alcohol dehydrogenase required for stage-specific floral organ  
RT abortion";  
RL Cell 74:757-768(1993).  
CC -!- FUNCTION: REQUIRED FOR STAGE-SPECIFIC FLORAL ORGAN ABORTION.  
CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases  
CC (SDR) family.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
CC EMBL; L20621; AAC37345.1; -.  
CC PIR; A47542; A47542.  
CC HSSP; P19992; 1HDC.  
CC MaizeDB; 56963; -.  
CC InterPro; IPR002198; ADH\_short.  
CC Pfam; PF00106; adh\_short; 1.  
CC PRINTS; PR00080; SDRFAMILY.  
CC PROSITE; PS00061; ADH\_SHORT; 1.  
CC Oxidoreductase; Developmental protein.  
CC NP\_BIND 59 83 NAD OR NADP (BY SIMILARITY).  
CC ACT\_SITE 207 207 BY SIMILARITY  
CC SQ SEQUENCE 336 AA; 35204 MW; 4E273D6152B0BB99 CRC64;

Query Match 42.2%; Score 588.5; DB 1; Length 336;  
Best Local Similarity 42.2%; Pred. No. 1.5e-39;  
Matches 122; Conservative 50; Mismatches 88; Indels 29; Gaps 4;  
Qy 5 TAFARRLEKGVALLTGASIGETAKLFSOHGAKVAIADVQDELGHSHVVEAIGTSNSTY 64  
Db 47 TPMPKRLDGVAVITVGARGIGEAIVRLFAGKHGVVIADIDDAAGALASALGPGQVS-F 105

```

QY 65 IHODVTNEDGVKNAVNTYSTY-GKLDIMFVNAGI---SDPNRPIIDNEKADPERVLSV 120
Db 106 VRCDSVEDDVRRAWDALSRGGRLDVTVCNNAGVLGRQTRAARSILSFDRAEEDRVLRV 165
QY 121 NVTGFLCMKHAARVMIPARSGNIISTASLSTMGSSSHAYCGSKHAYLATRNLAVAL 180
Db 166 NALGAALGKMKHAARAWAPRAGSIVSVASVAALVGLGPHFATSKAIAVLGLTKNAACEL 225
QY 181 GQFQIRVNCILSPRGLPTA-----LGKFTSGIKNEEPEFENVI 216
Db 226 RAHGVRVNCVSPRGVATPMLINAWRGCHDDATADADRLDLDTLDTVPDSQVEVKMEVV 285
QY 217 NFAGNLKGPKNVEDVANALYLASDEAKYVSGHNLFDIDGGFSVCNSVI 265
Db 286 RGLATLKGPTLRPRDIAEAVLFLASDEARYISGHNLVVDGGVTTSRNLI 334

RESULT 2
LINC_PSEPA
ID LINC_PSEPA STANDARD; PRT; 250 AA.
AC P50197;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE 2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase (EC 1.1.-.-)
DE (2,5-DIOL dehydrogenase).
GN LINC.
OS Pseudomonas paucimobilis (Sphingomonas paucimobilis).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Sphingomonas.
OX NCBI_TaxID=13689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UT26;
RX MEDLINE=94252977; PubMed=7515041;
RA Nagata Y., Ohtomo R., Miyauchi K., Fukuda M., Yano K., Takagi M.;
RT "Cloning and sequencing of a 2,5-dichloro-2,5-cyclohexadiene-1,4-diol
RT dehydrogenase gene involved in the degradation of gamma-
RT hexachlorocyclohexane in Pseudomonas paucimobilis.";
RL J. Bacteriol. 176:3117-3125(1994).
CC -1- FUNCTION: DEGRADATION OF 2,5-DICHLORO-2,5-CYCLOHEXADIENE-1,4-DIOL
CC (2,5-DDOL) INTO 2,5-DICHLORODROUINONE (2,5-DCHO).
CC -1- PATHWAY: Gamma-hexachlorocyclohexane degradation; third step.
CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC -----
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CC -----
DR EMBL; D14595; BAA03444.1; -.
DR HSSP; P19992; IHDC.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.
FT NP_BIND 9 34 NAD (BY SIMILARITY).
FT ACT_SITE 154 154 BY SIMILARITY.
SQ SEQUENCE 250 AA; 25644 MW; PFCICABE47DF789D CRC64;
Query Match 29.1%; Score 406; DB 1; Length 250;
Best Local Similarity 37.9%; Pred. No. 3.2e-25;
Matches 96; Conservative 42; Mismatches 103; Indels 12; Gaps 6;

QY 11 LEGKVALITGGAGIGETTKAFLSQHGAKVATADYQDELGHVSVVEIGTSGNSTVHCDDVT 70
Db 4 LSGKTIIVTGGSGIGRAITVELLVASGANVPVADINDGEAGEAVATSG-GKAAAFRCIDIA 62

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RESULT 3
YMPD_BACSU
ID YMPD_BACSU STANDARD; PRT; 255 AA.
AC P39640;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical oxidoreductase ympd (EC 1.-.-.-).
GN YMPD OR IPA-82D.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=95020537; PubMed=7934828;
RA Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W.,
RA Hullo M.F., Tonescu M., Lubochinsky B., Marcelino L., Mosser I.,
RA Presecan E., Santoni M., Schneider E., Schweizer J., Vertes A.,
RA Rapoport G., Danchin A.;
RT "Bacillus subtilis genome project: cloning and sequencing of the 97
RT kb region from 325 degrees to 333 degrees.";
RL Mol. Microbiol. 10:371-384(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Fekari E., Foulger D.,
RA Fritz C., Fujita M., Goffeau A., Gollightly E.J., Grandi G.,
RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Halesch J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Solido B.,
RA Sorokin A., Taccconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambit R., Wedler E., Wedler H., Weitzneger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus

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QY 71 NEDGVKNVNTYSTYCKLDIMFVNAGI---SDPNRPIIDNEKADPERVLSVNVTVGLCMK 130
Db 63 QEDVKAVALVACTIAAFGLDGSFNNAIQAQGLP-LAEVSLERFQSDMINDVTGFLCMK 121
QY 131 HAARWIP-ARSGNIISTASLSTMGSSSHAYCGSKHAYLATRNLAVALGQFQIRVNC 189
Db 122 YQILAMIERGTGKSGIVNTASAGVGVPMHGEYVGHAKHAVGLTRVAADYGRGIRNA 181
QY 190 LSPFGLPTALGKFPKSGIKNE---EEFENVINFAGNLKGPKNVEDVANALYLASDEAKY 246
Db 182 LVPQAVATPMLQR--AMNDNAGLEPYLINSIHPIGRFSEP---HEQAQAAVWLLSDAASF 235
QY 247 VSGHNLFDIDGGFS 259
Db 236 VTGSLAADGGFT 248

```

```
RT subtilis";
RL Nature 390:249-256(1997).
CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X73124; CAAS1638.1; -.
CC DR EMBL; Z99123; CAB15799.1; -.
CC DR PIR; S39737; S39737.
CC DR HSSP; P50162; IAE1.
CC DR Subtilisin; BG10628; ywED.
CC DR InterPro; IPR002198; ADH_short.
CC DR Pfam; PF00106; adh_short; 1.
CC DR PRINTS; PRO0080; SDRFAMILY.
CC DR PROSITE; PS00061; ADH_SHORT; 1.
CC DR Hypothetical protein; Oxidoreductase; Complete proteome.
CC KW NP_BIND 11 33 NAD OR NADP (BY SIMILARITY).
CC FT ACT_SITE 154 154 BY SIMILARITY.
CC SQ SEQUENCE 255 AA; 27324 MW; 20AA2259BFB88C9B CRC64;
Query Match 28.4%; Score 396; DB 1; Length 255;
Best Local Similarity 36.6%; Pred. No. 2e-24; 99; Indels 16; Gaps 4;
Matches 94; Conservative 48; Mismatches 99;
Qy 11 LEGKVALITGASGIGETTAKLFQHGAKVAIADVQDELGHVSVEAIGTSYIHCDVT 70
Db 5 LTDKTVLITGASGIGYAAVQAFLLQQANVVVADIDEAQGEAVRKNNDRHLHFQTDIT 64
Qy 71 NEDGVKNADVNTVSTYKGLDIFMSNAGIS--DPRNPRIIDNEKADFERVLVSVNVTGVFLC 128
Db 65 DEAAACQHAVESAVHTFGGLDVLINNAGIEIVAP----IHEMELSDWNKVLQVNLTMFLM 120
Qy 129 MKHAARVMIIPARSGNIISTASLSTMTGGSSHAYCGSKHVALTRNLAVELGQFGIRVN 188
Db 121 SKHALKMLAAGKNINTCVSGGLVAVPDIPATNASKGVLQUTKSNVAVDIKQHQIRVN 180
Qy 189 CLSPFGLPTALGKFKSGIKNEEFENV-----INFAGNLKPKFNVEDVANAALYLASD 242
Db 181 CVCFGIITPLNEKSFLENNEGTLEEIKKAKVNPILLRCKP----EEIANVWLFLASD 236
Qy 243 EAKTVSGHNLFDIGGFS 259
Db 237 LSSYMTGSAITADGGYT 253
RESULT 4
Y019_THEME
ID Y019_THEME STANDARD; PRT; 256 AA.
AC Q56318;
DT 01-NOV-1997 (Rel. 35, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DN Putative oxidoreductase TM0019 (EC 1.-.-.-).
GN TM0019.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
[1]
SEQUENCE FROM N.A.
STRAIN=MSB8 / DSM 3109;
MEDLINE=96125254; PubMed=8550425;
RA Kletzin A., Adams M.;
RT Molecular and phylogenetic characterization of pyruvate and 2-
RT keclovalerate ferredoxin oxidoreductases from Pyrococcus furiosus
RT and pyruvate ferredoxin oxidoreductase from Thermotoga maritima.;
RL J. Bacteriol. 178:248-257(1996).
```

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RN SEQUENCE FROM N.A.
RP STRAIN=MSB8 / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Hatt D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X85171; CAAS9459.1; -.
CC DR EMBL; AE001690; AAD35113.1; -.
CC DR PIR; E72427; E72427.
CC DR HSSP; O70351; 156W.
CC DR TIGR; TM0019; -.
CC DR InterPro; IPR002198; ADH_short.
CC DR Pfam; PF00106; adh_short; 1.
CC DR PRINTS; PRO0080; SDRFAMILY.
CC DR PROSITE; PS00061; ADH_SHORT; 1.
CC KW Hypothetical protein; Oxidoreductase; NADP; Complete proteome.
CC FT NP_BIND 9 33 NADP (BY SIMILARITY).
CC FT ACT_SITE 153 153 BY SIMILARITY.
CC FT CONFLICT 130 136 RGGGVII -> TRWRSDH (IN REF. 1).
CC SQ SEQUENCE 256 AA; 28078 MW; D68160B1D7980C6B CRC64;
Query Match 27.4%; Score 381.5; DB 1; Length 256;
Best Local Similarity 35.7%; Pred. No. 2.9e-23;
Matches 91; Conservative 54; Mismatches 99; Indels 11; Gaps 5;
Qy 11 LEGKVALITGASGIGETTAKLFQHGAKVAIADVQDELGHVSVEAIGTS--NSTYIHCD 68
Db 2 LEGKVAVVTGGQIGGIGNAIAQLFAENGKMKVIAIDEAGVEREEMLRERGLDVTFFKTD 61
Qy 69 VTNEDGVKNADVNTVSTYKGLDIFMSNAGISDPRNPRIIDNEKADFERVLVSVNVTGVFLC 128
Db 62 VADENSVMKVRKTVETIYGGVDVLNNAVMSVK--SIFERPLEEWERVIRVNLTPYIC 119
Qy 129 MKHAARVMIIPARSGNIISTASLSTMTGGSSHAYCGSKHVALTRNLAVELGQFGIRVN 188
Db 120 SRYCAEEMIKRGGGVIIINIASTRAFSQSEPDTEPYASKGGLVALTHSLAVSLSYHIRV 179
Qy 189 CLSPFGLPTALGKFKSGIKNEE--EPENVINFAAGLKPKNVEDVANAALYLASDE-AK 245
Db 180 SISFGWETSEWKKSLRKXPKDLPIDHEQHPAGRVGNPL----DIAHLCVFLADDEKAG 235
Qy 246 YVSGHNLFDIGGFSV 260
Db 236 FITGTNFIVDGGMTV 250
RESULT 5
LINUX_PSEPA
ID LINUX_PSEPA STANDARD; PRT; 250 AA.
AC P50198;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE 2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase (EC 1.1.-.-)
DE (2,5-DDOL dehydrogenase).
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Db 121 RAVKPMKEAGRSIIINSSIEGLAGTVACHGYTATKFAVRGLTKSTALELPGSGIRVNS 180
Qy 190 LSPFGL-----PTALGCKPSGKNBEEFENVINFAGNLKGPKFNVEDVANA 235
Db 181 IHP-GLVKTPTMDWPEDIFOTALGRAAEFPV-----EVSNL 215
Qy 236 ALYLASDEAKYVSGHNLFDGG 257
Db 216 VVYLASDESSYSTGAEFVVDGG 237

RESULT 7
FABG_THEME STANDARD; PRT; 246 AA.
AC Q9X248;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase).
GN FABG OR TM1724.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=9287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A., McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M., Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D., Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RA "Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of Thermotoga maritima.";
RT Nature 393:323-329(1999).
RL [2]
CC -|- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] + NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
CC -|- PATHWAY: Fatty acid biosynthesis pathway; first reduction step.
CC -|- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases (SDR) family.
CC
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CC
CC EMBL; AE001811; AAD36790.1; -.
CC PIR; H72219; H72219.
CC HSSP; P50162; 1AB1.
CC TIGR; TM1724; -.
CC InterPro; IPR002198; ADH short.
CC Pfam; PF00106; adh short; 1.
CC PRINTS; PR00080; SDRFAMILY.
CC PROSITE; PS00066; ADH_Short; 1.
KW Fatty acid biosynthesis; NADP; Complete proteome.
FT NP_BIND 10 34 NADP (BY SIMILARITY).
FT ACT_SITE 154 154 BY SIMILARITY.
SQ SEQUENCE 246 AA; 26401 MW; 8C08904D28039142 CRC64;

Query Match 26.1%; Score 363; DB 1; Length 246;
Best Local Similarity 35.8%; Pred. No. 8e-22;
Matches 91; Conservative 45; Mismatches 106; Indels 12; Gaps 6;

Qy 10 RLEKVALITGASGIGETITAKLSQHCARKVAIADVODE-LCHSVVFAIGTSNST--YIH 66
Db 2 RLEKVKLITGAASGIGKATTLFQAQEGATVIAGDISKENLDSLKAEGLPGKVDPYV- 60

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Qy 67 CDVTNEDGVKNAVDTVSTYTKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNTGVF 126
Db 61 LNVTRDQIKVEWEKVQYKIDVLVNNAGIT--RDALLVRMKEEDWDVAIVNVLKGVF 118
Qy 127 LCMKHAARVMIPARSGNIISTASLSSTMTGGSSSHAYCGSKHVLALTRNLAVELGQFGIR 186
Db 119 NVTQMVPVYMIKORNGSIVNVSSVVGIVYGNPGQNTYAAASKAGVIGMTKTWAKELAGNRIR 178
Qy 187 VNCISLPFGLPTALGCKPSGKNBEEFENVINFAGNLKGPKFNVEDVANAALYLASDEAKY 246
Db 179 VNAVAPGFETPTMTEKLPKARETALSRIIP--LGRFCKP-----EVAQVILFLASDESSY 232
Qy 247 VSGHNLFDGGFSV 260
Db 233 VTGQVIGIDGGLVI 246

RESULT 8
FABG_CHLPN STANDARD; PRT; 248 AA.
AC Q9Z8P2; Q9JQD1;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase).
GN FABG OR CPN0296 OR CP0462.
OS Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=101932388;
RA Kalman S., Mitchell W., Marathe R., Lamell C., Pan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RA "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RN [2]
CC -|- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] + NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
CC -|- PATHWAY: Fatty acid biosynthesis pathway; first reduction step.
CC -|- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases (SDR) family.
CC
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CC
CC EMBL; AE001811; AAD36790.1; -.
CC PIR; H72219; H72219.
CC HSSP; P50162; 1AB1.
CC TIGR; TM1724; -.
CC InterPro; IPR002198; ADH short.
CC Pfam; PF00106; adh short; 1.
CC PRINTS; PR00080; SDRFAMILY.
CC PROSITE; PS00066; ADH_Short; 1.
KW Fatty acid biosynthesis; NADP; Complete proteome.
FT NP_BIND 10 34 NADP (BY SIMILARITY).
FT ACT_SITE 154 154 BY SIMILARITY.
SQ SEQUENCE 246 AA; 26401 MW; 8C08904D28039142 CRC64;

Query Match 26.1%; Score 363; DB 1; Length 246;
Best Local Similarity 35.8%; Pred. No. 8e-22;
Matches 91; Conservative 45; Mismatches 106; Indels 12; Gaps 6;

Qy 10 RLEKVALITGASGIGETITAKLSQHCARKVAIADVODE-LCHSVVFAIGTSNST--YIH 66
Db 2 RLEKVKLITGAASGIGKATTLFQAQEGATVIAGDISKENLDSLKAEGLPGKVDPYV- 60

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OM protein - protein search, using sw model

Run on: October 23, 2003, 12:45:14 ; Search time 97 Seconds  
(without alignments)  
726.272 Million cell updates/sec

Title: US-09-673-918A-2  
Perfect score: 1393  
Sequence: 1 MQLTAFARRLEKGVALLTG.....IDGFSVCNSVIKVFQYPS 273

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID        | Description        |
|------------|-------|-------------|--------|-----------|--------------------|
| 1          | 1364  | 97.9        | 277    | 10 Q94KL7 | Q94kl7 forsythia i |
| 2          | 734   | 52.7        | 267    | 10 P93697 | P93697 vigna ungui |
| 3          | 700.5 | 50.3        | 271    | 10 Q94G09 | Q94g09 cucumis sat |
| 4          | 695   | 49.9        | 274    | 10 Q8H0D9 | Q8h0d9 phaseolus l |
| 5          | 693.5 | 49.8        | 271    | 10 Q94G10 | Q94g10 cucumis sat |
| 6          | 685   | 49.2        | 284    | 10 Q50038 | C50038 nicotiana t |
| 7          | 677   | 48.6        | 284    | 10 Q82465 | Q82465 ipomoea tri |
| 8          | 673   | 48.3        | 277    | 10 Q9SBD8 | Q9sbd8 ipomoea tri |
| 9          | 670   | 48.1        | 284    | 10 Q9SBD6 | Q9sbd6 ipomoea tri |
| 10         | 668   | 48.0        | 277    | 10 Q9SBD7 | Q9sbd7 ipomoea tri |
| 11         | 665.5 | 47.8        | 273    | 10 Q9SBM0 | Q9sbm0 citrullus l |
| 12         | 658.5 | 47.3        | 285    | 10 Q9C826 | Q9c826 arabidopsis |
| 13         | 652.5 | 46.8        | 278    | 10 Q94KL8 | Q94kl8 podophyllum |
| 14         | 625.5 | 44.9        | 303    | 10 Q9SCU0 | Q9scu0 arabidopsis |
| 15         | 597.5 | 42.9        | 283    | 10 Q9ZK17 | Q9zr17 arabidopsis |
| 16         | 593.5 | 42.6        | 259    | 10 Q93V47 | Q93y47 digitalis l |

# ALIGNMENTS

RESULT 1

|    |                                                                     |              |      |         |
|----|---------------------------------------------------------------------|--------------|------|---------|
| ID | Q94KL7                                                              | PRELIMINARY; | PRT; | 277 AA. |
| AC | Q94KL7;                                                             |              |      |         |
| DC | 01-DEC-2001 (TREMBLrel. 19, Created)                                |              |      |         |
| DT | 01-DEC-2001 (TREMBLrel. 19, Last sequence update)                   |              |      |         |
| DT | 01-MAR-2003 (TREMBLrel. 23, Last annotation update)                 |              |      |         |
| DE | Stem secolisolaricresinol dehydrogenase (Fragment).                 |              |      |         |
| OS | Forsythia intermedia (Border forsythia).                            |              |      |         |
| OC | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  |              |      |         |
| OC | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;        |              |      |         |
| OC | Asteridae; lamids; Lamiales; Oleaceae; Forsythia.                   |              |      |         |
| OX | NCBI_taxid=55183;                                                   |              |      |         |
| RN | [1]                                                                 |              |      |         |
| RP | SEQUENCE FROM N.A.                                                  |              |      |         |
| RX | MEDLINE=21201084; PubMed=11278426;                                  |              |      |         |
| RA | Xia Z.Q.; Costa M.A.; Pellissier H.C.; Davin L.B.; Lewis N.G.;      |              |      |         |
| RT | "Secoisolaricresinol Dehydrogenase Purification, Cloning, and       |              |      |         |
| RT | Functional Expression. IMPLICATIONS FOR HUMAN HEALTH PROTECTION."   |              |      |         |
| RL | J. Biol. Chem. 276:12614-12623 (2001).                              |              |      |         |
| CC | !- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES |              |      |         |
| CC | (SDR) FAMILY.                                                       |              |      |         |
| DR | EMBL: AF352735; AAK38665.1; -                                       |              |      |         |
| DR | InterPro; IPR002198; ADH_short.                                     |              |      |         |
| DR | Pfam; PF00106; adh_short; 1.                                        |              |      |         |
| DR | PRINTS; PR00080; SDRFAMILY.                                         |              |      |         |
| DR | PROSITE; PS00061; ADH_SHORT; 1.                                     |              |      |         |
| FW | Oxidoreductase.                                                     |              |      |         |
| KT | NON TER 277                                                         |              |      |         |
| SQ | SEQUENCE 277 AA; 29256 MW; 98885C210CAFE2EB CRC64;                  |              |      |         |

Query Match 97.9%; Score 1364; DB 10; Length 277;

Best Local Similarity 98.2%; Pred. No. 2.5e-95;

Matches 267; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 QLRTAFARRLEKGVALLTGASGIGETAKLFSGHGAKVAIADVQDELGHVWEAIGTSN 61

Db 6 QVLTAIARRLEKGVALLTGASGIGETAKLFSGHGAKVAIADVQDELGHVWEAIGTSN 65

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QY 62 STYIHCDVTNEDGVKNVADNTVSTYKGLDIMPFSNAGISDPNRPRIIDNEKADPERVLSVN 121
DB 66 STYIHCDVTNEDGVKNVADNTVSTYKGLDIMPFSNAGISDPNRPRIIDNEKADPERVLSVN 125
QY 122 VTGVFLCMKHAARVMIIPARSGNIISTASLSSTMTGGSSHAYCGSHAVLALTRNLAVELG 181
DB 126 VTGVFLCMKHAARVMIIPARSGNIISTASLSSTMTGGSSHAYCGSHAVLGLTRNLAVELG 185
QY 182 QFGIRVNCISPFGLPTALGCKKSGIKNEEFENVINFAGNLKGPKFNVEDVANALYLAS 241
DB 186 QFGIRVNCISPFGLPTALGCKKSGIKNEEFENVINFAGNLKGPKFNVEDVANALYLAS 245
QY 242 DEAKYVSGHNLFTDGGFSVCNSVIKVFQYDPS 273
DB 246 DEAKYVSGHNLFTDGGFSVCNSVIKVFQYDPS 277

RESULT 2
P93697 PRELIMINARY; PRT; 267 AA.
AC P93697;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE CPRD12 protein.
OS Vigna unguiculata (Cowpea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX NCBI_TaxID=3917;
RN [1]
SEQUENCE FROM N.A.
RA Iuchi S., Yamaguchi-Shinozaki K., Urao T., Shinozaki K.;
RT "Characterization of two cDNAs for novel drought-inducible genes in
RT the highly drought-tolerant cowpea.";
RL J. Plant Res. 109:415-424(1996).
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; D88121; BAAL3541.1; -.
DR HSSP; P19992; IHDC.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase.
SQ SEQUENCE 267 AA; 28484 MW; 8C4A4A2E9F41B64 CRC64;

Query Match 52.7%; Score 734; DB 10; Length 267;
Best Local Similarity 56.3%; Pred. No. 1,1e-47;
Matches 147; Conservative 41; Mismatches 67; Indels 6; Gaps 2;

QY 9 RLREGKVALITGASGIGETTAKLFSOHGAKVAIADVODELCHSVVEAIGTSYIHC 68
DB 12 KRLREGKVALITGASGIGETTAKLFSOHGAKVAIADVODELCHSVVEAIGTSYIHC 69
QY 69 VTNEDGVKNVADNTVSTYKGLDIMPFSNAGISDPNRPRIIDNEKADPERVLSVNVTGVFLC 128
DB 70 VTKEEDIEKCVDTAVSKFKGLDIMPFSNAGISDPNRPRIIDNEKADPERVLSVNVTGVFLG 129
QY 129 MKHAARVMIIPARSGNIISTASLSSTMTGGSSHAYCGSHAVLALTRNLAVELGQFGIRVN 188
DB 130 TKHAARVMIIPARSGNIISTASLSSTMTGGSSHAYCGSHAVLGLTKTNVAVELGQFGIRVN 189
QY 189 CLSPFGLPTALGCKKSGIKNEEFENVINFAGNLKGPKFNVEDVANALYLASDEAKYVS 248
DB 190 CVSPFPAITVPLLNKYFNLEDEGVKRTKMYMLKGVVPPV---NDVAEALYLASDESKFVS 245
QY 249 GHNLFIDGGFSVCNSVIKVFQ 269
DB 246 SHNLVIDGGGLINSNVGFPWF 266

RESULT 3
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Q94G09 PRELIMINARY; PRT; 271 AA.
AC Q94G09;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Sex determination protein.
OS Cucumis sativus (Cucumber).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OX NCBI_TaxID=3659;
RN [1]
SEQUENCE FROM N.A.
RA Sun J.-Q., Li Q.-Z., Li X.-G.;
RT "Gene cloning and expression of CSG in cucumber.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AF286651; AAK83036.1; -.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase.
SQ SEQUENCE 271 AA; 28997 MW; 7CD6ED7F52AD6224 CRC64;

Query Match 50.3%; Score 700.5; DB 10; Length 271;
Best Local Similarity 53.7%; Pred. No. 3.7e-45;
Matches 146; Conservative 44; Mismatches 75; Indels 7; Gaps 4;

QY 1 MQLTAPARRLEGKVALITGASGIGETTAKLFSOHGAKVAIADVODELCHSVVEAIGTS 60
DB 3 IQLPAPARRLEGKVALITGASGIGETTAKLFSOHGAKVAIADVODELCHSVVEAIGTS 62
QY 61 NSTYIHCDVTNEDGVKNVADNTVSTYKGLDIMPFSNAGISDPNRPRIIDNEKADPERV 118
DB 63 SSVFVHCDVTKEKDVETAVDTAVSKYKGLDIMPFSNAGISDPNRPRIIDNEKADPERV 121
QY 119 SVNVTGVFLCMKHAARVMIIPARSGNIISTASLSSTMTGGSSHAYCGSHAVLALTRNLAV 178
DB 122 NVNLVGAFGLTKHAARVMIIPARSGNIISTASLSSTMTGGSSHAYCGSHAVLALTRNLAV 181
QY 179 ELGQFGIRVNCISPFGLPTALGCKKSGIKNEEFENVINFAGNLKGPKFNVEDVANAL 237
DB 182 DLGRYGVNCVSNVVPVTEMGRKLPKVDGGGEP--SFYWSLKNGLDILREEDVGEAVV 238
QY 238 YLASDEAKYVSGHNLFTDGGFSVCNSVIKVFQ 269
DB 239 YLGSDESKVCSGLNLIVDGGFTVNVQALCSFR 270

RESULT 4
Q8H0D9 PRELIMINARY; PRT; 274 AA.
AC Q8H0D9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Alcohol dehydrogenase.
OS Phaseolus lunatus (lima bean) (Phaseolus limensis).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
OX NCBI_TaxID=3884;
RN [1]
SEQUENCE FROM N.A.
RA Horiuchi J., Arimura G., Ozawa R., Muroi A., Takabayashi J.,
RA Nishioaka T.;
RT "Phaseolus lunatus ";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
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[illegible]

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RESULT 7
ID 082465 PRELIMINARY; PRT; 284 AA.
AC 082465;
DT 01-NOV-1998 (TEMBLrel. 08, Created)
DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Short-chain alcohol dehydrogenase.
GN SSP.
OS Ipomoea trifida.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Convolvulaceae; Ipomoea.
OX NCBI_TaxID=35884;
RN [1]
SEQUENCE FROM N.A.
RA Koyama Y., Kadota N., Sassa H., Kakeda K., Tsuchiya T., Ishimizu T.,
RA Kondo K., Norioka S.;
RT "S-locus specific stigma protein (SSP) from sporophytic self-
RT incompatibility plant, Ipomoea trifida, is a member of short-chain
RT alcohol dehydrogenase family.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AF072447; AAC35340.1; -.
DR HSSP; P19992; IHDC.
DR InterPro; IPR002198; ADH short.
DR Pfam; PF00106; adh short. 1.
DR PRINTS; PR00080; SDRFAMILY.
DR Oxidoreductase.
KW Oxidoreductase.
SQ SEQUENCE 284 AA; 29823 MW; 4C04A888178C0633 CRC64;

Query Match 48.6%; Score 677; DB 10; Length 284;
Best Local Similarity 51.9%; Pred. No. 2.4e-43;
Matches 135; Conservative 41; Mismatches 84; Indels 0; Gaps 0;

QY 8 ARLEGKVALITGASGIGETTAKLFSQHGAKVAIADVODELGHVSVEAIGTSNVTYIHC 67
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 67
DB 11 SKLEGKVAITITGAANGIGATTARLFAHQGCKVIIADIDKNGHSAVEEIGPEYALFIHC 70
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 70

QY 68 DVNEDGVKNADVNTYSTYTKGLDIFMSNAGISDPNRPRIIDNEKADFERVLSVNVTVGVFL 127
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 127
DB 71 DVRIESDVQNAVDTTVTSRYGKLDIFMSNAGVAGSRDTSILEASPENINLVFETNVFGAFF 130
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 130

QY 128 CMKHAARVMIPARSGNIISTASLSSTMTGGSSHAYCGSKHVALTRNLAVELGQFGIRV 187
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 187
DB 131 CAXHAARVMIPARKGSVIFSASAASEVFGITSDTYTASCAVVGKSLCVMGKYGIKA 190
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 190

QY 188 NCLSPGLPTALGKFKFSIKNEEFENVINPAGNLKGPKNVEDVANAALYLASDEAKYV 247
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 247
DB 191 NCVSPVILTKLWSIMPTQDKLAEIIVAEASNFKGKLTITTEDVAEALYLAGDESKFV 250
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 250

QY 248 SGHNLFDGGFSVCNSVVKV 267
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 267
DB 251 SGLNLLIDGGFTTTNTAFQV 270
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 270

RESULT 8
ID 09SBD8 PRELIMINARY; PRT; 277 AA.
AC 09SBD8;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE Short-chain alcohol dehydrogenase.
GN SSP.
OS Ipomoea trifida.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Convolvulaceae; Ipomoea.
OX NCBI_TaxID=35884;
RN [1]
SEQUENCE FROM N.A.
RA Koyama Y., Kadota N., Sassa H., Kakeda K., Tsuchiya T., Ishimizu T.,
RA Kondo K., Norioka S.;
RT "S-locus specific stigma protein (SSP) from sporophytic self-
RT incompatibility plant, Ipomoea trifida, is a member of short-chain
RT alcohol dehydrogenase family.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AF072448; AAC35341.1; -.
DR HSSP; P19992; IHDC.
DR InterPro; IPR002198; ADH short.
DR Pfam; PF00106; adh short. 1.
DR PRINTS; PR00080; SDRFAMILY.
DR Oxidoreductase.
KW Oxidoreductase.
SQ SEQUENCE 277 AA; 29312 MW; 7A75BEEF12A73D9AE CRC64;
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RP SEQUENCE FROM N.A.
RA Koyama Y., Kadota N., Sassa H., Kakeda K., Tsuchiya T., Ishimizu T.,
RA Kondo K., Norioka S.;
RT "S-locus specific stigma protein (SSP) from sporophytic self-
RT incompatibility plant, Ipomoea trifida, is a member of short-chain
RT alcohol dehydrogenase family.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AF072448; AAC35341.1; -.
DR HSSP; P19992; IHDC.
DR InterPro; IPR002198; ADH short.
DR Pfam; PF00106; adh short. 1.
DR PRINTS; PR00080; SDRFAMILY.
DR Oxidoreductase.
KW Oxidoreductase.
SQ SEQUENCE 277 AA; 29312 MW; 7A75BEEF12A73D9AE CRC64;

Query Match 48.3%; Score 673; DB 10; Length 277;
Best Local Similarity 51.7%; Pred. No. 4.6e-43;
Matches 134; Conservative 42; Mismatches 83; Indels 0; Gaps 0;

QY 9 RRLEGKVALITGASGIGETTAKLFSQHGAKVAIADVODELGHVSVEAIGTSNVTYIHC 68
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 68
DB 12 KRLEGKVAITITGAANGIGATTARLFAHQGCKVIIADIDKNGHSAVEEIGPEYALFIHC 71
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 71

QY 69 VTNEDGVKNADVNTYSTYTKGLDIFMSNAGISDPNRPRIIDNEKADFERVLSVNVTVGVFLC 128
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 128
DB 72 VRIESHVQHAVDTTVTSRYGKLDIFMSNAGVAGSRDTSILEASPENINLVFETNVFGAFFC 131
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 131

QY 129 MKHAARVMIPARSGNIISTASLSSTMTGGSSHAYCGSKHVALTRNLAVELGQFGIRVN 188
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 188
DB 132 AKHAARVMIPARKGSVIFSASAASEVFGITSDTYTASCAVVGKSLCVMGKYGIKAN 191
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 191

QY 189 CLSPGLPTALGKFKFSIKNEEFENVINPAGNLKGPKNVEDVANAALYLASDEAKYVS 248
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 248
DB 192 CVSPVILTKLWSIMPTQDKLAEIIVAEASNFKGKLTITTEDVAEALYLAGDESKFVS 251
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 251

QY 249 GHNLFDGGFSVCNSVVKV 267
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 267
DB 252 GLNLLIDGGFTTTNTAFQV 270
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 270

RESULT 9
ID 09SBD6 PRELIMINARY; PRT; 284 AA.
AC 09SBD6;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE Short-chain alcohol dehydrogenase.
GN SSP.
OS Ipomoea trifida.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Convolvulaceae; Ipomoea.
OX NCBI_TaxID=35884;
RN [1]
SEQUENCE FROM N.A.
RA Koyama Y., Kadota N., Sassa H., Kakeda K., Tsuchiya T., Ishimizu T.,
RA Kondo K., Norioka S.;
RT "S-locus specific stigma protein (SSP) from sporophytic self-
RT incompatibility plant, Ipomoea trifida, is a member of short-chain
RT alcohol dehydrogenase family.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AF072450; AAC35343.1; -.
DR HSSP; P19992; IHDC.
DR InterPro; IPR002198; ADH short.
DR Pfam; PF00106; adh short. 1.
DR PRINTS; PR00080; SDRFAMILY.
DR Oxidoreductase.
KW Oxidoreductase.
SQ SEQUENCE 284 AA; 29898 MW; 2B54BFFBAD6BAE4A CRC64;
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Query Match      48.1%; Score 670; DB 10; Length 284;
Best Local Similarity 51.7%; Pred. No. 8.1e-43;
Matches 134; Conservative 41; Mismatches 84; Indels 0; Gaps 0;

QY 9 RRLGKVALITGGASGIGETTAKLFSQHGAKVAIADVDQDELGHSHVVEAIGTSNSTYIHCD 68
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
12 KRLGKVALITGAANGIGATTARLFAQHGCKVIAIDDDKNGHSAVEIGPEYALFIHCD 71
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 69 VTNEDGVKNAVNTVSTYKGLDIFMFSNAGISDPNRPRIIDNEKADFVRLSVNVTGVFLC 128
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 72 VRIESVQNAVDTTVSRYGKLDIFMFSNAGVAGSRDTSILEASPNINLVFETNVFGAFC 131
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 129 MKHAARVMIIPARSGNIISTASLSSTMGSGSHAYCGSKHVALTRNLAVELQFGIRVN 188
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 132 AKHAARVMIIPARKGSVIFSAASAASEVFGITSDTYTASKCAVVGKSLCVMGKYGIKAN 191
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 189 CLSPFGLPTALGKFKSGIKNEEFENVINPAGNKGPKFNVEDVANAALYLASDEAKYVS 248
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 192 CVSPYVILTKLGMIMPTQDKLAEIIVAEASNFKGKTLTTEDVAAEALYLAGDESKFVS 251
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 249 GHNLFIDGFGFVCNSVIKV 267
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 252 GLNLLIDGGFTTNTAFQV 270
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
Q9SBD7 ID Q9SBD7 PRELIMINARY; PRT; 277 AA.
AC Q9SBD7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Short-chain alcohol dehydrogenase (S-locus linked stigma protein)
EN SSP OR SSP10
OS Ipomoea trifida.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamiales; Solanales; Convolvulaceae; Ipomoea.
OX NCBI_TaxID=35884;
RN [1]
RP SEQUENCE FROM N.A.
RA Koyama Y., Kadota N., Sassa H., Kakeda K., Teuchiya T., Ishimizu T.,
RA Kondo K., Norioka S.;
RT "S-locus specific stigma protein (SSP) from sporophytic self-
RT incompatibility plant, Ipomoea trifida, is a member of short-chain
RT alcohol dehydrogenase family.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=H77-2;
RC Tsuchiya T., Suabe K., Wataae T., Kagaya Y., Koyama Y.;
RT "Characterization of promoter region of the SSP gene from Ipomoea
RT trifida regulates stigma-specific expression.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AF072449; AAC35342.1; -.
DR EMBL; AB070221; BAB86916.1; -.
DR HSP; P19992; IHDC.
DR InterPro; IPR002198; ADH short.
DR Pfam; PF00106; adh short; 1.
DR PRINTS; PR00080; SDRFAMILY.
KW Oxidoreductase.
SQ SEQUENCE 277 AA; 29257 MW; AOCDB434B31C666D CRC64;

Query Match      48.0%; Score 668; DB 10; Length 277;
Best Local Similarity 51.7%; Pred. No. 1.1e-42;
Matches 134; Conservative 41; Mismatches 84; Indels 0; Gaps 0;

QY 9 RRLGKVALITGGASGIGETTAKLFSQHGAKVAIADVDQDELGHSHVVEAIGTSNSTYIHCD 68
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 12 KRLGKVALITGAANGIGATTARLFAQHGCKVIAIDDDKNGHSAVEIGPEYALFIHCD 71
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 69 VTNEDGVKNAVNTVSTYKGLDIFMFSNAGISDPNRPRIIDNEKADFVRLSVNVTGVFLC 128
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 72 VRIESVQNAVDTTVSRYGKLDIFMFSNAGVAGSRDTSILEASPNINLVFETNVFGAFC 131
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 129 MKHAARVMIIPARSGNIISTASLSSTMGSGSHAYCGSKHVALTRNLAVELQFGIRVN 188
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 132 AKHAARVMIIPARKGSVIFSAASAASEVFGITSDTYTASKCAVVGKSLCVMGKYGIKAN 191
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 189 CLSPFGLPTALGKFKSGIKNEEFENVINPAGNKGPKFNVEDVANAALYLASDEAKYVS 248
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 192 CVSPYVILTKLGMIMPTQDKLAEIIVAEASNFKGKTLTTEDVAAEALYLAGDESKFVS 251
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 249 GHNLFIDGFGFVCNSVIKV 267
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 252 GLNLLIDGGFTTNTAFQV 270
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
Q9SBD7 ID Q9SBD7 PRELIMINARY; PRT; 273 AA.
AC Q9SBD7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Wt62L.
GN WTS2L.
OS Citrullus lanatus (Watermelon) (Citrullus vulgaris).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Citrullus.
OX NCBI_TaxID=3654;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim J., Kang H., Jun S., Lee J., An G.;
RT "Cloning of three gibberellin-regulated cDNAs from watermelon during
RT early seed development: down-regulated one cDNA and up-regulated two
RT cDNAs.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AB018559; BAA89230.1; -.
DR HSP; P19992; IHDC.
DR InterPro; IPR002198; ADH short.
DR Pfam; PF00106; adh short; 1.
DR PRINTS; PR00080; SDRFAMILY.
KW Oxidoreductase.
SQ SEQUENCE 273 AA; 28835 MW; 904A835DD52B6E2 CRC64;

Query Match      47.8%; Score 665.5; DB 10; Length 273;
Best Local Similarity 51.1%; Pred. No. 1.7e-42;
Matches 137; Conservative 48; Mismatches 74; Indels 9; Gaps 4;

QY 9 RRLGKVALITGGASGIGETTAKLFSQHGAKVAIADVDQDELGHSHVVEAIGTSNSTYIHCD 68
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 11 RRLDGKVALITGGASGIGTSVAVRIFHENGAKVIAIDQDEIGQKIADELG-DDVSIYHCD 69
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 69 VTNEDGVKNAVNTVSTYKGLDIFMFSNAGISDPNRPRIIDNEKADFVRLSVNVTGVFLC 128
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 70 VSKEDDVSNLVDAAVHRHGKLDIMYSNAGVLDLDFSGILDVTKSLDKVLGVNVMGAFWG 129
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 129 MKHAARVMIIPARSGNIISTASLSSTMGSGSHAYCGSKHVALTRNLAVELQFGIRVN 188
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 130 AKHAARVMIIPKNGCILFTSSATTNTAGLSSHYPYAAKCAVLGLVRLNLAELQHGIRVN 189
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 189 CLSPFGLPTALGKFKSGIKN---EEEFENVINPAGNKGPKFNVEDVANAALYLASDEAK 245
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 190 CVAPFVVATGI---AGSRDPMQAEALETWTTWNLKGRVLKADDIKAAALYLASDDAN 245
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 246 YVSGHNLFDIGGFSVCN-SVIKVFQYPD 272
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 246 YVSGNLVVDGGYVSVNPTMLKTLKMD 273
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 12  
 Q9C826 PRELIMINARY; PRT; 285 AA.  
 ID Q9C826;  
 AC Q9C826;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Short chain alcohol dehydrogenase, putative (Short-chain  
 dehydrogenase/reductase).  
 GN F19K6.3 OR ABA2 OR ATIG52340.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;  
 OC Eurosid II; Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=5702;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=21016719; PubMed=1130712;  
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,  
 RA White O., Alonso J., Altaki H., Araujo R., Bowman C.L., Brooks S.Y.,  
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,  
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,  
 RA Dunn P., Egu P., Feildlyum T.V., Feng J.-D., Fong B., Fujii C.Y.,  
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,  
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,  
 RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,  
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,  
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,  
 RA Militecher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,  
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
 RA Sakano H., Salzer S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,  
 RA Unterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,  
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;  
 RA "Sequencing and analysis of chromosome 1 of the plant Arabidopsis  
 thaliana";  
 ET thaliana";  
 RL Nature 408:816-820 (2000).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RA Cheng W.-H., Endo A., Zhou L., Penney J., Chen H.-C., Arroyo A.,  
 RA Leon P., Nambara E., Asami T., Seo M., Koshiba T., Sheen J.;  
 RA "A unique short-chain dehydrogenase/reductase in Arabidopsis glucose  
 signaling and abscisic acid biosynthesis and functions";  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 [3]  
 RP SEQUENCE FROM N.A.  
 RA Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,  
 RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,  
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,  
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,  
 RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,  
 RA Ecker J., Theologis A., Davis R.W.;  
 RA Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 (SDR) FAMILY.  
 CC EMBL; AC037424; AAG51536.1; -;  
 DR EMBL; AY082344; AAL99237.1; -;  
 DR EMBL; AY082345; AAL99238.1; -;  
 DR EMBL; AY095603; AAM20454.1; -;  
 DR HSP; P29132; IDFI  
 DR InterPro: IPR002198; ADH short.  
 DR Pfam: PF00106; adh short; 1.  
 DR PRINTS; PR00080; SDRFAMILY.  
 DR PROSITE; PS00061; ADH\_SHORT; 1.  
 KW Oxidoreductase.  
 SQ SEQUENCE 285 AA; 30272 MW; 8B555DAED7386DF4 CRC64;  
 Query Match 47.3%; Score 658.5; DB 10; Length 285;  
 Best Local Similarity 50.9%; Pred. No. 6e-42; Mismatches 13; Gaps 5;  
 Matches 139; Conservative 43; Indels 13;

QY 8 ARLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSHVVEAI--GTSNST-- 63  
 DB 15 SORLLGKVALITGGATGIGESIVRLFKHGAKVCIVLQDDLGGEVCKSLRGSKETAF 74  
 QY 64 YHCDVTNEDGVKNADVNTSTYKGLDIFMFSNAGISDPNRPRIIDNEKADFVLSVNVVT 123  
 DB 75 FHGDVVRVEDDISNADVDFAVKNFGTDLILINAGLCGAPCPDIRNYSLSSEFEMTFDYNVK 134  
 QY 124 GVFLCMKHAARVMI PARSGNIISTASLSSTMTGGSSSHAYCGSKHVLALTRNLAVELGQF 183  
 DB 135 GAFLSMKHAARVMIPEKKGSIVSLCSVGVGVGVPHSYVSGSKHVLGLTRSAALGQH 194  
 QY 184 GIRVNCLSFGFLPTALGKKFGSKINEEFENVI---NFA---GNLKGPKFNVEDVANAA 236  
 DB 195 GIRVNCVSPYAVATKLA--LAHLPEERTEDAFVGRFNAANANLKGVELTVDDVANAV 252  
 QY 237 LYLASDEAKYVSGHNLFIIDGGFVSNVSVIKYQF 269  
 DB 253 LFLASDDSRYSISGDNLMIDGGFTCTNHSFKVFR 285  
 RESULT 13  
 Q94KL8 PRELIMINARY; PRT; 278 AA.  
 ID Q94KL8;  
 AC Q94KL8;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Rhizome secoisolariciresinol dehydrogenase (Fragment).  
 OS Podophyllum peltatum (Mayapple).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;  
 OC Berberidaceae; Podophyllum.  
 OX NCBI\_TaxID=35933;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21201084; PubMed=11278426;  
 RA Xia Z.Q., Costa M.A., Pelissier H.C., Davin L.B., Lewis N.G.;  
 RA "Secoisolariciresinol Dehydrogenase Purification, Cloning, and  
 Functional Expression. IMPLICATIONS FOR HUMAN HEALTH PROTECTION";  
 RL J. Biol. Chem. 276:12614-12623 (2001).  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 (SDR) FAMILY.  
 CC EMBL; AF352734; AAK38664.1; -;  
 DR InterPro: IPR002198; ADH short.  
 DR InterPro: IPR000205; NAD\_binding.  
 DR Pfam: PF00106; adh short; 1.  
 DR PRINTS; PR00080; SDRFAMILY.  
 DR PROSITE; PS00061; ADH\_SHORT; 1.  
 KW NON TER 278  
 SQ SEQUENCE 278 AA; 29253 MW; DB735A376E112375 CRC64;  
 Query Match 46.8%; Score 652.5; DB 10; Length 278;  
 Best Local Similarity 52.2%; Pred. No. 1.7e-41;  
 Matches 133; Conservative 43; Mismatches 76; Indels 3; Gaps 3;  
 QY 10 RLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSHVVEAIGTSN-STYIHC 68  
 DB 13 RLQDKVAIITGGAGGIGETTAKLFSYKGVKVIADIDHGHQKVCNNIGSPDVISFVHCD 72  
 QY 69 VTNEDGVKNADVNTSTYKGLDIFMFSNAGISDPNRPRIIDNEKADFVLSVNVTVGFLC 128  
 DB 73 VTKDEDVRLVDTTIAKHGKLDIMEFNGVGLSTTTPSYILEAGNEDFKRVMDINVYGAFLV 132  
 QY 129 MKHAARVMI PARSGNIISTASLS--TMGGGSHAYCGSKHVLALTRNLAVELGQFGRV 187  
 DB 133 AKHAARVMI PAKGSI VFTTASISSSTAGEGVSHVYATKHAIVGLTSLCTELGEYGRV 192  
 QY 188 NCLSPGLTALCKKPSGIGKNEEFENVINPAGNKPKFNFVEDVANALVLADEAKYV 247  
 DB 193 NCVSPFIVASPLTDFGV--DSRVEELAHQAANLKLRAEDVADNAVAYLAGDESKYV 251

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Qy 248 SGHNLFDGGSVCN 262
Db 252 SGLNLVDGGVTRTN 266

RESULT 14
Q9SCU0 PRELIMINARY; PRT; 303 AA.
AC Q9SCU0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Short-chain alcohol dehydrogenase-like protein.
GN T18N14.60.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN 1
RP SEQUENCE FROM N.A.
RA Habermann K., de la Bastide M., Huang E.N., Gnoj L., Schutz K.,
RA Preston R., Calma C., Martienssen R., Parnell L.D., Dedhia N.,
RA McCombie W.R.;
RT "Arabidopsis thaliana BAC F4C21 from chromosome IV near 17 cM.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN 2
RP SEQUENCE FROM N.A.
RA Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M.,
RA Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M.,
RA Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N.,
RA Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN 3
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AC005275; AAD14442.1; -.
DR EMBL; AL161496; CAB77799.1; -.
DR HSP; P19992; IHDC.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase.
SQ SEQUENCE 283 AA; 29994 MW; 93B0A97CECC859BC CRC64;

Query Match 42.9%; Score 597.5; DB 10; Length 283;
Best Local Similarity 47.0%; Pred. No. 2.4e-37;
Matches 126; Conservative 45; Mismatches 86; Indels 11; Gaps 4;

Qy 9 RRLEKVALITGASGIGETAKLFQSHGAKVAIAVDQDELGHVSVEAIGTSYIHCD 68
Db 16 RKLEKVALITGASGIGETAKLFQSHGAKVAIAVDQDELGHVSVEAIGTSYIHCD 74
Qy 69 VTNEDGVKNADVNTVSTYGLDIFMSNAGISDPNRPRIIDNEKADPERVLSVNVGVFLC 128
Db 75 VTKESDIANADVFAVSLHTKLDIMYNNAGIPCKTPPSIVDLNVPDKVINTNVRGVMA 134
Qy 129 MKHAARVMIIPARSGNTIISTASLSSTMGSSSHAYCGSKHVALTRNLAVELGQFIRVN 188
Db 135 IKHAARVMIIPRNSGSIICAGSVTGMGGLAQHTYSVSKSAVIGIVRSTASELCKHRIRVN 194
Qy 189 CLSPFGLPTA-----LGKPSGINKBEEFPENVINFAGNLKGPKPNVEDVANAALYLASDE 243
Db 195 CISPPFAITTSFVMDENRQIYPGV-DDSRLTIQIVQSTGVNLNGVECEPTDVANAALYLASDD 253
Qy 244 AKVSGHNLFDGGSVCNVIKVFQYP 271
Db 254 SKYVGNHNLVVDGGF-----TTVKTLDPP 277

Search completed: October 23, 2003, 12:50:40
Job time : 101 secs

Qy 5 TAFARLEKVALITGASGIGETAKLFQSHGAKVAIAVDQDELGHVSVEAIGTSYST- 63
Db 26 TLTPKRLKVALITGAGHIGKATVLFARHGATVVIADVNDVAGSLAKSSSHKTSP 85
Qy 64 ---YIHCVTNEDGVKNADVNTVSTYGLDIFMSNAGISDPNRPRIIDNEKADPERVL 118
Db 86 MVAFISCDVSEADVNLVNVTVARYGRDLILFNNAVGLDQKKHKSILDFDADEFDHYM 145
Qy 119 SVNVTGVFLCKHARVMIIP-ARSGNIISTASLSSTMGSSSHAYCGSKHVALTRNL 177
Db 146 RVNRYGVGLGMKHGARAMIKRGFKGCIISTASVAGVMGGMGPHTAYTASKEAIVGLTKNAA 205
Qy 178 VELGQFIRVNCISLSPFLPTAL-----GKFTSG--IKNE--EPEFNVINFAGNLKGPKFNV 229
Db 206 CELGKIRVNCISLSPFGVATSMVNWARKTSGGVDDEDDVEEMEEFVRSANLKGKTLRA 265
Qy 230 EDVANAALYLASDEAKTVSGHNLFDGGSVCNVI 265
Db 266 NDIAEALYLASDESKYVGNHNLVVDGGVITARNVCV 301

RESULT 15
Q9ZR17 PRELIMINARY; PRT; 283 AA.
AC Q9ZR17;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative alcohol dehydrogenase.

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